

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Gatanaga, T.
Granger, G.A.

(ii) TITLE OF INVENTION: Factors Altering Tumor Necrosis
Factor Receptor Releasing Enzyme Activity

(iii) NUMBER OF SEQUENCES: 154

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: MORRISON & FOERSTER
(B) STREET: 755 PAGE MILL ROAD
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304-1018

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: Windows
(D) SOFTWARE: FastSEQ for Windows Version 2.0b

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: USSN 09/081,385
(B) FILING DATE: 014-NOV-1998

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME:
(B) REGISTRATION NUMBER:
(C) REFERENCE/DOCKET NUMBER: 22000-20577.21

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 650-813-5600
(B) TELEFAX: 650-494-0792
(C) TELEX: 706141

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4047 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAGCTTTTG	CTTCTTCC	CCGGAAAGG	CCGGGGCCAG	AGACCCGAC	TCGGACCAGG	60
CGGGGGCTGC	GGGGCCAGAG	TGGGCTGGG	AGGGCTGGGA	GGGCGTCTGG	GGCCGGCTCC	120
TCCAGGCTGG	GGGGCGCCAG	CTCCGGGAAG	GCAGTCCTGG	CCTGCGGATG	GGGCGCGCG	180
TGGGGCCCGG	CGGGGCGGCC	TGGGAGGGCC	TCCAGGCTGC	GGGAGGGGGA	GGAGCGCCCG	240
TGGGGCCGCC	AGGGCCGTGG	GTGGAGGTGCG	CCGTCCCTCC	TGAGGGGCAG	CCAGTGCGTT	300
TGGGACCCGG	GACGAGAGCC	CGCGCCTCCC	CAGCGGCCTC	CCCGGGGGTC	TCACCGGGTC	360
ACCCGAGAGC	GGAGGGCCCG	GCTCCGCAGA	AACCCGGGGC	GGCCGGGGGG	AAGCAGGCC	420
CTCAGGCGTC	GGAGGAGGCC	CCAGAAAGGAC	CTCGCGCCTT	CCCGCCGGGC	TCCGACCGCC	480
TGGGTTCCGT	GGGGGACGGC	CCAGGGCGCC	AGGACCCCCA	AGCCGAGCTC	AGCTGCGGG	540
GCACGACCCA	GAGGCCAGCA	GCAGAGGACG	GGGCGGGGGC	CGGGAGAGGG	CGGGGAGGGC	600
GCTCTGGG	GGTCAAGGCC	AGGGCTAGAC	TTTCAGGGTC	ATGGCCTGGC	CCCTCATCCC	660
CAGGGAGGTG	AGGGGGCTCT	GTGAGCAGAG	GGGGCCCCGG	TGGAGAAGGC	GCTGCTAGCC	720

AGGGGGCGGGG	CAGGAGCCCA	GGTGGGGACT	TAAGGGTGGC	TGAAGGGACC	CTCAGGCTGC	780
AGGGATAGGG	AGGGAAAGCTA	GGGGTGTGGC	TTGGGGAGGT	GCTGGGGGAC	CGCGGGCGCC	840
CTTTATTCTG	AAGCCGAATG	TCCTGCCGGA	GTCCCCAGTG	ACCTAGAAAT	CCATTTCAAG	900
ATTTTCAAGG	GTTCAGCTG	GAGACAAAGG	CCAGGCCAG	GTAAAAATGT	GGCAGTGACA	960
GAGTATGGG	TGAGAACAC	GGAGAGAGGA	AGTCCCCGAG	GCGGATGATG	GGACAGAGAG	1020
CGGGGACCAAG	AATTTTTAA	AACGCATCTG	AGATCGTGT	GGCAGACTCA	TAGTTGTTT	1080
CCTTCACGG	AGAAAGTGTG	GGCAGAAGCC	AGCTCTAAAG	CCCAGGCTGC	CCAGCCTGCA	1140
CTGGCAGAGC	TGACGGAAGG	CCAGGGCAGA	GCCTTCCCTC	CCTGTCACAG	ACATGAGCCC	1200
TGGAGATCTG	GAATGAGGCA	GATGTGCCCA	GGGAAGAGCTG	ATCCTCCCCC	ACCCAGGGCC	1260
CCCCGGTGC	CCCTTGTAGC	GTGGAATCGT	TGCCAGGTCA	TGGCTCCCTG	CTATCGAAC	1320
CCGGACACGG	GTGCTGTGCT	GCACCTGGCA	GTTGAGGAC	CGACACCCAC	AATGCCTTAA	1380
GAGGTGATGA	CTGCCTTCCA	GGGGCCTGGC	TGGCTGACAC	TTTGCATGGC	TCCTGGAGAA	1440
GAGGGATTGA	GTGGAGTCCA	CGGGTCACTG	CCACCTCCTG	GGTCTGCTC	CTGAGGGCAGG	1500
GCCCCGCTGG	GGTGGAGAAGG	GGCTGGAGAC	AGGTTCTCTG	CAGTTCAACCC	TCTAACCGGT	1560
GGTCTTCATG	CCTAGGAAC	CACTGGGGGC	TTATGAAACT	GCAGGTGGCT	GAGTCCTTGC	1620
CATGGGGTCT	CTCCTTCAGG	AGGTCTGGGT	GGGGCCGGAG	ACTGACCCC	ACAAAGGGTC	1680
CCAGGTGAGG	CGGAGATGTGC	CTGGCGCTGT	GTGGCTCTGG	ACCTAGTCTC	TGGGCTTGGG	1740
CTGGCCTCCA	GGGCCTGGGC	TTGAGACAGC	TGTGACGCA	GCAAGCCATT	TACCCCGTT	1800
GTGGGGACAT	TACATCTTCC	TAGCTGGAA	CACACAGGCA	GCCAGGGTGT	TTATCCACAT	1860
TCCCTCTCCA	TGTTCTTC	TTGAGAACTT	TTACCAAGTA	TGTCAAGGAC	TGGGCTCCAC	1920
CAGGGAGACT	CAAGTGGAAA	GGCCCTCATCC	TGTGCTCCA	GGAGACAGGA	AAACCTATGG	1980
TTACAATTCC	AGGGACAAGA	GGCATGCA	TGAGGTGTGG	CAAATCTCAC	TGTTCAACTG	2040
GAGAAAATCAG	AGACAGCTTC	CTGGAGGCAG	TGACACCTGG	ACAGGCTCT	CCACAGGAGG	2100
AAGGGAGTGA	GAGAAGCCAA	CTGGGATGGA	CCCATCATGT	AGGGGAAACA	GTGCGCCGAG	2160
AACCAACAAAC	ACCCCCCACC	CTAGGCCAG	AGCTCACGGA	GAGAGCTGGG	CCTCTCGGGG	2220
TGACTACATA	GTTCCTCTGCT	GGATCTTAGG	TCTGCTCTT	GGGCAGCTCT	GCTGAGACCT	2280
CTATGCCTGT	TCCAGGCTGC	ACCAAGGTTT	TGTGACTATT	GGTCTGGGGT	TGTTTGCAG	2340
CAACTGAAGT	GTTCCTGTTG	AAAACAGGCA	CTTGATTGTC	TGAAAGGAAT	GCTGTTTGT	2400
CTTGCCTCGA	CAAACATTGA	GCAGCACTTA	GTGGGCGTT	TATATCTGT	GGAGTAATGG	2460
GTGTTTCTG	AGTCTGTCTG	GGGTACTGCA	CATTTAAAGG	AAATCATTT	TCTGAAACAT	2520
TGCTATTTC	CAACACAGAA	ATCATATCC	TCTGCTGTC	CATGTCTGAA	GACCTTACAC	2580
GAGAAAAGTCT	TAATGTAAGT	TTAGTAGAGT	CCTTGGATGG	AGAAACTAATT	ATATCATACA	2640
TTGCCGCTTT	CTCACTCTGC	TCTTTTCAT	CCTTGCCTAA	TTTCATTTC	TTCTGCTTCT	2700
TTTGTGTTCT	TTCTGGAGAA	TCTAGCAAGA	TATCTGGG	AAACATCTGA	GGTGTGAAC	2760
AAGGTAGAGA	CTGAGATTGT	AGGATTAAGG	GTGGCTTG	GCCTTAAAGG	GTTCTTCAC	2820
TTCCAGCAGG	GGAGCATACT	GGCTGTGAG	ATCTCACGGG	AAAAGATGCA	GCATTCCTCA	2880
TTGGTGAAGG	ATCTCCATCG	TCACTACTTA	GGCTGTGCA	CATGTGTAGG	TAGTCTTCAC	2940
TTGAACCATG	TCTAGGATTA	TCAGCATGAT	GATTAGCTGA	ATTGCCAGAC	AACGGACCAAG	3000
AAACTTTATT	ATCATGTATG	TTTCTCAAAC	CACCTGCAAC	AATGGGACTT	GATACCGATG	3060
CTTGTGTCAT	CTGTGAGTGT	GTGTTGTAAC	TTGAAGGATG	GGAATATGGC	ATGTATCTG	3120
CAGGGCTTTG	TGGGGCGTAT	GGACTAGGCA	CTGGGTATT	TTGCTGTGGC	ATAAAATCTGT	3180
TCCCAGAGCT	TGTCCTGTGGT	GGCACAAACC	GGCTGGAGGG	GCTATGTGAG	ATAGTGGTT	3240
GTTGATAATT	GGAAGATGCA	GGACTACTGT	GCATGGAATT	CTGAGAAAGT	TTATACTGAG	3300
ACATCATCAT	TCCACTTTG	ACATATCTGT	TCTGCTGTC	TTTCTCTCG	AAAACATTAG	3360
GACTCCTTC	CAGGACGGCC	TGCAACAAAGA	CTGGTATGTC	ACCTTCTGGG	TCATCACTGC	3420
CAAGGTATTC	TTTCAACTCT	ATGTGATCTG	TTGATACCTG	GTGAGGCTA	TGGACAAGCT	3480
GTGAACACAA	ATTGTCATCC	CTACAAGCCA	AAAGGCAGTT	CACCTCTCT	GCTATTCTG	3540
CATTAAAGAG	AAGGCTCTT	GTAGTTGAG	CAGGTAAGG	AGATGGAAGA	GGCAGCTGTT	3600
TCAGGAGGTC	TGTGAGACTA	GCAATCCCCG	CAAGAGTAGT	AATGGGGACA	TGGGGCATAT	3660
CCCCATTCT	CTCTGAAATTTC	TGGAATGGTG	TTGCTCTAA	AAGTACTTAG	TTCAGGTGCC	3720
AGCTGTCTT	ACTTCCCATT	TCCCAAAAC	TGGGGCAATC	GGCGCTGCAA	TCCAAGGGGA	3780
GGCCGAGGCC	GCTGTGGCGA	GAGACTATAA	TCCGGGCCGG	GAGGGGGGGC	GGCTACGGCT	3840
CCTCTCCCTG	CTCCCTAGTG	CGGGGAACAT	GTAGAGCCCG	GGGGAGACCA	GCCGAGAAGA	3900
CAAATCGTTG	CTTCTCTTC	CTCCCTCTCC	TCCTTCCTCC	ACATAGAAC	ACTCACAAAC	3960
ACCCGACCAAC	GGGGCCGAGC	TACCGGGGGG	GCATCGCCGC	GGGGCCGGGA	ACCAATTCTC	4020
CTGTCGGCGG	GGGCGTCTT	TGGATCC				4047

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 739 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGATCCAAG	GTCAAACCTCC	CCACCTGGCA	CTGCCCCCG	AGCGGGTCGC	GCCCCGGCCGG	60
CGCGCGGCCG	GGGCCCTTGGC	GCCAGAAGCG	AGAGCCCCCTC	GGGGCTCGCC	CCCCCGCCTC	120
ACCCGGTCA	TGAAAAAAAC	ATCAGAGTAG	TGGTATTCA	CCGGGGCC	GCAGGGCCGG	180
CGGACCCCGC	CCCCGGCCCC	TCGCGGGGAC	ACCGGGGGGG	CGCCGGGGGC	CTCCCACTTA	240

TTCTACACCT	CTCATGTCTC	TTCACCGTGC	CAGACTAGAG	TCAAGCTAA	CAGGGTCTTC	300
TTTCCCCGCT	GATTCGGCCA	AGCCCGTCC	CTTGGCTGTG	GTTTCGCTGG	ATAGTAGGTA	360
GGGACAGTGG	GAATCTCGTT	CATCCATTCA	TGCGCGTCAC	TAATTAGATG	ACGAGGCATT	420
TGGCTACCTT	AAGAGAGTC	TAGTTACTCC	CGCCGTTAC	CCGCGCTTCA	TTGAATTTC	480
TCACTTGAC	ATTCAAGAGCA	CTGGGCAGAA	ATCACATCGC	GTCACACCCC	GCCCGGGGCC	540
TTCGGGATGC	TTTGTTTAA	TTAACACGT	GSATTCCCCT	GGTCCGCACC	AGTTCTAAGT	600
CGGCTGCTAG	GCGCCGGCCG	AAGCGAGGCG	CCGCGCGGAA	CCGCGGGCCC	CGGGGGCGAC	660
CCGGGGGGGG	GACCGGGCCG	CGGGCCCTCC	GCCGCCTGCC	GCCGCCGCC	CCGCGCGCG	720
CCGAAGAAGA	AGGGGGAAA					739

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAAGAGTGGC	GCGCCGAGCA	GGCCCCCGG	GTGCCCCGGC	CCCCCTCGAG	GGGGACAGTG	60
CCCCCGCCCG	GGGGGGCCCG	CGGCGGGCCG	CCGCCGGCCC	CTGCCGCCCC	GACCCTTCTC	120
CCCCCGCCGC	CGCCCCCACG	CGGCGCTCCC	CCGGGGAGGG	GGGAGGACGG	GGAGCGGGGG	180
AGAGAGAGAG	AGAGAGAGGG	CGCGGGGTGG	CTCGTGCCTGA	ATTCAAAAG	CTT	233

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGATCCAAG	AATTCCGGAC	GAGGTAGTCA	CGGCTCTTGT	CATTGTTGA	CTTGACGTTG	60
AGGCTGGTA	GCTTGGAAA	GTCGATGCGC	AGCGTGACG	AGGCGTTGA	GATGTTCTGC	120
CCGTCAGCG	ACAGCTTGGC	GTGCTGGCG	CTCACGGGGT	CCGCATACTG	CAGCAGGCC	180
TGGAACCTGGT	TGTTCTTGGT	GAAGGTGATG	ATCTTCAACA	CTGTGCCAA	CTTGGAGAAA	240
ATCTGGTCA	GCACATCCAG	GGTCACAGGG	TAGAAGAGGT	TCTCCACGAT	GATCCTGAGC	300
ACGGGGCTCT	GCCCCGCCAT	CGCCATCCCT	GCATCCACGG	CCGCGCCGA	GGCAGCCAAG	360
GCCAGGTCTC	CCGACTGGAC	CGAGGTACCC	GCCTGCAGGG	CCGCGCTGGC	CCGCGCCCTGG	420
TTGGAGAGC	TGTCGGTCTT	CACTCTCTTG	TGGTTGGAGA	ACTGGATGA	GATGGGCTGG	480
CCGGCGAGCA	CAGGGGTCA	CGAGGTGAG	TAGTTACCA	TGGTATTGGC	AGCCTCCCTC	540
GTGTTCATCT	CGATGAAGGC	CTGGTTTTTC	CCCTTCAGCA	TCAGGAGGT	GTTGACCTTC	600
CCAAAGGGCA	GCCCCAGGGA	GATGACTTCC	CCCTCCGTA	CGTCGATGG	GAGCTTCCGG	660
ATGGGATCA	CTCTAGAGGG	GACGCCCTCA	CTTCGGCTG	CACCTTGA	CTTCTTGTG	720
TCATTTCCGT	TTGCTGCAGA	AGCCGAGTTG	CTGCTCATGA	TAACCGTCC	TTAGTGACA	780
CAACTAGAGA	AAAGCTCGTC	AGATCCCGC	TTTGTACCAA	CGGCTATATC	TGGGACAATG	840
CCGTCATGC	CACACAGAGC	AGACCCCGG	GGGACGGAGT	GGAGGCCGCG	GAATCCTGGA	900
GCTAGAGCTG	CAGATTGAGT	TGCTGCCTGA	GACGAAGCG	AAGTATGAGA	GTGTCCTGCA	960
GCTGGGCCG	GCACAGACAG	CCCACCTTA	CAGCCTGCTG	CAGACCCAGC	ATGCACCTGGG	1020
TGATGCCCTT	GCTGACCTCA	CGCAGAACGT	CCACAGACTT	CAGGGAGGA	TTGGCTACAA	1080
TGCAAGAGCA	CAGAAACTAC	TATGCAAGAA	TGGGAAACG	CTGCTAGGAG	CCGTGAACCT	1140
CTTTGCTCT	AGCATCAACA	CATTGGTCAC	CAAGACCATG	GAAGACACGC	TCACTGACTGT	1200
GAACAGTAT	GAGGCTGCCA	GGCTTGGAA	TGATGCCAC	CGAACAGACT	TAGAGGAGCT	1260
GAGTCTAGGC	CCCCGGGATG	CAGGGACAC	TGGTCGACTT	GAGAGTGGCC	AGGCCACTTT	1320
CCAGGCCCCAT	CGGGACAAGT	ATGAGAACGT	GGGGGGAGAT	GTGGCCATCA	AGCTCAAGTT	1380
CCTGGAAAGAA	AACAAAGATCA	AGGTGATGCA	CAAGCAGCTG	CTGCTCTTCC	ACAATGCTGT	1440
GTCGGCTAC	TTTGCTGGGA	ACCAGAAACA	GCTGGAGCAG	ACCCCTGCAGC	AGTTCAACAT	1500
CAAGCTGCGG	CCTCCAGGAG	CTGAGAAACC	CTCCCTGGCTA	GAGGAGCAGT	GAGCTGCTCC	1560
CAGCCCCAACT	TGGCTATCAA	GAAGACATT	GGGAAGGGCA	GCCCCAGGGT	GTGGGAGATT	1620
GGACATGGTA	CATCCTTGT	CACTTGGCTT	CTGGCTTGGG	CTCCCTTTTC	TGGCTGGGGC	1680
CTGACACCAAG	TTTGCCCCAC	ATTGCTATGG	TGGGAAGAGG	GCCTGGAGGC	CCAGAAAGTT	1740
CTGCCCTGTC	TATCTTCTG	GCCACAGGGC	TTCATTCCTA	GATCTTTCC	TTCCACCTCA	1800
CAGCCAACGG	CTATGACAAA	ACCACTCCCT	GGCCAATGGC	ATCACTCTC	AGGCTGGGGT	1860
GTCCTCCCTG	ACCAATGACA	GAGGCTGAAA	ATGCCCTGTC	AGCCAAATGGC	AGCTCTTCTC	1920
GGACTCCCT	GGCCCAATGA	TGTTGCGTCT	AATACCCCTT	GTCTCTCTC	TATGCGTGCC	1980
CATTGCGAG	AAGGGGACTG	GGACCAAAGG	GGTGGGGATA	ATGGGGAGCC	CCATTGCTGG	2040

CCTTGCATCT	GAATAGGCCT	ACCCTCACCA	TTTATTCACT	AATAACATTT	ATTTGTGTT	2100
TCTAATTAA	AATTACCTT	TCATCTTGT	TGATTTTCT	TCAGCTAAAT	TAGAAATTG	2160
TAGTTTTCC	CCTAAAAAAAT	TCAATGGCAT	TCTTCTTAT	AAATTACATT	CTCTGATTT	2220
CTTGTCAGCC	TGCTTCAGG	AAATCCATGT	GTTCAAAATG	CTTGCTCCCA	GTTTGCTCCA	2280
TACCAAATGG	TTGCTTAACC	CAAATATCTG	AGCAGCAAT	TGAGCTGATC	CTTCTGGAGA	2340
AAGTACGGTT	GAACAGCCAA	GACCACTGGG	TAGTCGAAGA	GAAGACCCAA	CATCCTGAC	2400
TCCCCAGTCT	GGTGTGAGGG	GAGGACAGCT	GATAACTGGA	TATGCACTGT	TCCCAGACAT	2460
CACTGGTCCC	AAACCATTAC	TTCTGCCCTGC	CACTGCCACA	AATAACAGTAG	GAATGCCATC	2520
CCCTTCATAC	TCAGCTTAA	TCCCTCAGAGT	TTCATCTGGT	CTTTATGCCG	CAGATGTTAC	2580
TGGAAGTCA	CATGGATGCA	CAAATTTCC	ACAGGCCCTTC	TGATTTTTT	CACAGTGACC	2640
AAGATCAGAA	GTAGAGGCCA	TCAACACTAC	AACCCCTGAC	TGACTTTCTG	ATTTAAAAG	2700
CAACTCTACT	CTCTCTGCAA	CCCACTCAA	GTTTTCTTT	ACCATTGGA	GCCCTTCAGG	2760
AGTTACTCT	TTGAGGGTCCC	GATAAGACTG	TTTGTCTTC	TGTTGGCTTC	GATCTCCTGA	2820
TGGCCAGAGT	CTCCAGGAAT	CATTGTCAAT	AACATCAGCA	AGAACAAATT	CTTTGGTGGT	2880
TACATCAACA	CCAAATTCAA	TCTTCATATC	AACCACTGTA	CAATTCTGGG	GCAACCAGGA	2940
TTTCTCAGT	ATTCAAATA	TAGCCGTGT	AGCATCTCGT	GCCGAATTCA	AAAAGCTT	2998

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AAGCTTTTG	TGAAACACCT	AGGATATGTC	CCCTCCCTCA	CCACACCCAA	CCCCCGGCC	60
CTGCCCCAGG	ACATGACGAT	GCCTCACACA	CACACACACA	CACACATACA	CACAAGGGCG	120
TGAGCTGCAC	GCAGGAACAT	GGGCTGCACT	CACGACAACA	TTGAAAAAAAT	ATACATTATA	180
TATGTACACC	CGGGGCCCCC	ACGTCCCCTC	CCGTCCCCGC	AGCCTGCCA	CACCAGGTCA	240
CGGAGGAGGG	GCCGGGGCTG	CAGGACCTCA	GGACTGCAAG	GGCAGGAAGG	GAAACAGGAC	300
AAGAAAGGAA	GGAAGTGGAA	AAGGAGGGAG	AAATGGGGTC	CCAGAGACTGA	AATGGAAATG	360
AGGTGGGGCG	ATCATAAGAG	AAGCAGGGAC	GATGGTCCAG	CTGAGGGAGC	CCTGCAGAGG	420
GGGAAAGGCT	TCCCATGGAC	AGGAGAGAGA	AGGGAAGGGG	AGAGGGAGGG	GTTTCCCTCA	480
ATCCCACCCC	CAGCCCCAGC	CCCAGCCCCA	GCCATTGCAA	TGTCACCCCT	CTCCCCAACAA	540
CAGTGAATGTC	TAAGGGGCA	GCTGCCATTG	GGGGTAGAAA	GGCAGCTGAA	GTCCAGCCCCA	600
CTTTCAACCA	CAGCAGCCC	CAGTCAAGG	GGCACACCAG	GAGCATGACA	GCCCAGAACG	660
GAGGGATGGG	GGGGCGGGGG	AGGGGCAAGG	CGGACTCTCAG	AGGGCCGGCT	GGGGTTTGA	720
AATGAAAGGA	GGACTGGTTC	TGAAGCCTCT	CTCCCTCTTG	GTCTCTGTG	TCCCAGAAAG	780
TCCTTCCTCC	ATGTCCTGG	TCTCTGTTC	ACCAGGGCAG	AATTCCCCCT	CTGCAGGG	840
AGAGGTGAG	GCCTTAGTAG	CGGTGTGGGG	GGGTGATGGT	GATGCGCTC	TCGTCGCTG	900
TGGGGGAAATC	GGCCACCTTC	GAGTCACTGC	TGTCCTCATC	CTCCTGCTGG	CCCCCAACAG	960
CCCCCGTCAC	ACAGGACTGC	CGATTCTGTT	AGGACTCTCA	GGGGTTCA	ATGATGGTGA	1020
GAGCTGAGTC	ATCCCAGAAG	AGGTCTGGGT	CCTTGGGGTC	ACTGGAGGCC	CCTGGAGGCC	1080
CGCCGGCCCC	TGAGACCGGG	CGGTGAAGGG	AATGGATGCC	CACCAGGCC	AGGACGACCA	1140
TGAGCACCAAG	GAAGGCCAAC	CACCCACAA	TGATGAGGGT	TGGCGCGCTG	GTATCATGG	1200
AGTTCTGTG	GGAGCTGGTC	AGGCTGTGTC	CAGCCATCTC	AGGGGGGGG	TGTTGACCA	1260
GCTGCAGGAA	CTGCTGGGG	CTGAGCAGGT	GGCTGGGGT	GGCAACCCGG	TTCATGCTG	1320
GCAGGACATT	GACCTCCACG	ATGAATTATC	TGCTGGAGTA	ACGGCCATT	ATTCCGAGC	1380
AGGAAAGCCG	GAACCTTCTG	GTGAGGAGGG	CAGCTCCCTG	TCGCAGGCCA	TAACGAGCT	1440
GCCTCAGGAT	CTCTTCATAC	ACAGTGTGTC	TCTCCACCCC	ACCAATAGTG	AGTAGGGCAG	1500
ATGTGTTGGT	GAGCTCCAGC	CCCCGCTGCT	CGAGAGAGGT	TGTCAGGCC	AGCAGGCTTT	1560
CCCGCTCGGG	ATCCAGGTCA	TCCCCACCA	GAGAAATTTC	ACAGCCATCC	AGGTGTGCA	1620
CAATCTCATC	CGACATGCGT	GTGCTGTCA	CTGTGCCCTG	CCAACTCTCA	TCCTTTTGG	1680
CCTCCACCTG	GTGAGAAATG	GAGCAGGTGA	TTTGAAGATC	AGGGAAACAA	GGCACGCCGT	1740
TGTTTCCCTC	AAAGTCCACA	GCTGGCGGG	CAAATATGAC	AGTGCACATC	AGCAGGACT	1800
GGGGGGCGGT	AGGGTGAAGG	ACGACCACTG	AGCCCTCCAC	TTCAGGATG	GAGACGCCAG	1860
ACTCTTCGCT	GAAGCACTTG	ACAGCAGTGG	TGAGGGCAG	GGGCTGACG	CCGGCCGTGG	1920
CAAAGCGAG	AGTGTTCATG	TAAGCCACAT	GCTGCAGGGC	ATGGTTGAAG	GTCTCCACAT	1980
CATCCCCCTC	CAGGGTGAAGC	AGGGACTGTG	AGGGGTTCAC	GTGGACCTTC	ATGCTTTGC	2040
CCAGGCTCTC	GAATCCCTA	TAGTCAGG	CCTCCCGACA	TGCTAGAGG	CACTCGATGA	2100
CCTCGCGGCT	CTCCAGGGCA	CCTGAGCGCA	CGCTGAAACC	AGCCAGGTAG	CCATGGAAGT	2160
AGTGTGTTGAT	CGCAAAGGG	TCTCTTGGG	TGGTGTCTG	ACTGTTGTCT	CCCTTTTCT	2220
TCTCTTGTG	CTTCTCCCTCA	GTCCAGCAGG	CCCCAATCAT	GAGAGCAGGC	TCCCTTCGGG	2280
GTGGGGGGAT	GAGGCCATTG	TGATGGATGA	GGGCAAGGGC	GAAGGGAGATG	CCGTCGGTAT	2340
AGAGTGTGAC	TGTTGGGAAAC	TGAGGGTCA	GGCGCTAGTG	GTGCCACTCA	TCATCACAGA	2400
CCTGCTCCAG	CTTCCAGAGG	AACCTGACTG	GGCGGGCACT	CTCAAGCAGG	GGCCAGTAGA	2460
GGAAGGCAAT	CCTACAGCCG	TGAGCAGTCA	GGCAGTAGTG	AGAGAAAGCCG	TCCTCATCT	2520
GGACAGTGT	ACATACGATG	GTTCCTCTT	CTTCTTGCC	CTTGTGGGA	GTACGCCAT	2580
GCTTCATCCA	GAAGGACAGG	GTGAAGTGTG	CACTGAGGCT	GTCCCTGGGC	CCAGACCCA	2640

GCCCCACTGGG	GCCACCCAGG	GGCACCTGCA	CAGCCTGGGT	GCCATTGAAC	CAGTAGATCA	2700
GGCTGCTGTC	CTGGCTGTAG	TGCACCGAGA	GTCTGCTGT	CCAGTGTGCA	TTGGGGCCAG	2760
GCATGGGCAA	CAGATCCACT	TCCCCAGTGG	CAGCACCACA	AGGTTTCCGC	AGCGCCCCGCT	2820
CTGAGTAGTT	GTCACGGTCA	CAGCCCTGG	CCACCATGGCT	GTCCTGCGC	TCTATGGTGG	2880
CCTGAATGTT	CCAGAGTGGT	TCATCACAGG	TCTCCAGCG	GATACCAGGG	AACAAAGCCA	2940
AGCTCCCAGC	ACCTGGTCA	TATTCGATCC	TTTGTCCA	GCCTTGCCAG	CTGGGTTTAC	3000
AGGTGGGCTT	CACCTGAATC	TCCACCTCG	CATCATCTGC	TGCCCGCTTC	TTCCCACAGT	3060
CATAAGCTGT	CACTGTAAAC	TTATAGAGGC	TCTCACCACT	GTACTGCGC	TTCTCTGTGT	3120
TCTCAATGTT	CCCGTCATTG	TCATAGGAGA	AAGGGGTGTT	GGGTGTGAGA	ATCTCATAGT	3180
AGCAGATCTG	GCTGTACTGG	GGGGAGCAGT	CACCGTAAT	GCCTTCCACC	CGCAGGATGC	3240
GATCGTACAG	CTTCCCCCT	GTCACAGCG	CACGATACAG	CCGTTCCACA	AAACACTGGGG	3300
CAAACCTGTT	CACATCGTTG	ACCCGACAT	GCACAGTGGC	CTTGTGGAC	TTCTTGGTGT	3360
TGGCCCCGTC	GGGGCCCTCG	CCACAGTCAT	AGGCTGGAT	GGTGAAGGTG	TGTTCTCTT	3420
GGGCTCGCA	GTCCCACAGG	TCTTGGCC	GGATCAGGCC	CTTCTCTGTC	GCCTTGTCAA	3480
GGATCACAGC	CTCAAAAGGC	ACCCAGACG	CATGGAGCG	GAAGCCGCAG	ATCTCACCTG	3540
CATAGCGCAG	CGGGGCATCC	TTGTTCAAGG	CAAAGAGTGG	TGGATTCACT	AGGACCGTGT	3600
TGTCAATTCTC	CATGACGATG	CCCTGGTACT	CTGCTCAAT	CCATGGCTTG	TGCTTGTGG	3660
CTTTGTTACA	GGAGCAGGAC	GCGAGCAGAG	AGGCCAGCAG	AAGGGGCAGC	AGCAGGAGGG	3720
TCATGGTGC	GGCTGGGGCA	GGGGCAGGC	AGGCGTTGG	CTTCCCTGGG	AGCCTCCAGC	3780
CTGCGGATTC	CACCTTGGCG	GAGGGATACA	GGGGGGAAA	ACCAAAATAA	AACGTCAAAT	3840
AAATTGTGTA	GGAGGGAGTCC	AGCTTAGGAC	CGGGCCAGAG	CCAGGCCAGG	CTCGGGGAGG	3900
GGGCCTCTGC	AGGTTCAAGG	GATCACTGCT	GCCACCAACG	CCACCCCTGG	AGCCAGTTAT	3960
TTTGGCATGG	CCTTGATTGC	AACAGTGGC	TCCCTCTGTCA	TGGCAGACAG	CACCGTGTAC	4020
AGGATCTCTT	CTCACAGTC	GTACTCTGC	TCATCTCCT	TGCCAAGGTC	TCCCTCAGGG	4080
AGACGAAGGT	CCTCTCGTAC	CTCCCCGCTG	TCCTGGAGCA	GTATAGGTA	CCCATCCTGG	4140
ATCTTGGAT	CC					4152

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGATCCAAAG	ATTCGGCACG	AGTGGCCACA	TCATGAACCT	CCAGGCCCC	CCCAAGGCTC	60
AGAACAAAGC	GAAGCGTTGC	CTCTTGGGG	GCCAGGAACC	AGCTCCCAAG	GAGCAGCCCC	120
CTCCCCCTGCA	GCCCCCCCCAG	CAGTCCATCA	GAGTGAAGGA	GGAGCAGTAC	CTCGGGCAGC	180
AGGGTCCAGG	AGGGGCAGTC	TCCACCTCTC	AGCTGTGGT	ACTGCCCCCT	CCTAGCAGCC	240
TGGCCCTGCT	GAACCTCTGT	GTGTATGGC	CTGAGCGGAC	CTCAGCAGCC	ATGCTGTCCC	300
AGCAGGGTGC	CTCAGTAAAG	TGGCCAACT	CTGTGATGGC	TCCAGGGCGG	GGCCCGGAGC	360
GTGGAGGAGG	TGGGGGTGTC	AGTGACAGCA	GCTGGCAGCA	GCAGCCAGGC	CAGCCTCCAC	420
CCCATTCAAC	ATGGAACACTG	CACAGTCTGT	CCCTCTACAG	TGCAACCAAG	GGGAGCCCCC	480
ATCCTGGAGT	GGGAGTCCCG	ACTTACTATA	ACCAACCTGA	GGCACTGAAG	CGGGAGAAAAG	540
CGGGGGGCCA	ACAGCTGGAC	CGCTATGTC	GACCAATGAT	GGCCAGCAGAAG	GTGAGCTGG	600
AGGTAGGGCG	GGCCCGAGCA	CCCCCTGAATT	CTTCCACAGC	AGCCAAGAAA	CCCCCAAACC	660
AGTCACTGCC	CCTGCAACCC	TTCCAGCTG	CATTGGCCA	CCAGGTGAAC	CGGCAGGTCT	720
TCCGGCAGGG	CCCACACCCC	CCAAACCCGG	TGGCTGCC	CCCTCCACAG	AAGCAGCAGC	780
AGCAGCAGCA	ACCACAGCAG	CAGCAGCAGC	AGCAGCAGGC	AGCCCTACCC	CAGATGCCG	840
TCTTGTGAA	CTTCTATTCC	ATGCCACAGC	AACCCCTCGCA	GGAAACCCAG	GACTTTGGCC	900
TGCAGCCAGC	TGGGGCACTG	GGACAGTCCC	ACCTGGCTCA	CCACAGCATG	GCACCCCTACC	960
CCTTCCCCCC	CAACCCAGAT	ATGAACCCAG	AACTGCGAA	GGCCCTTCTG	CAGGACTCTAG	1020
CCCCCGCAGC	AGCGCTACCT	CAGGCCAGA	TCCCTCTCC	CCGGCGCTCC	CGCCGGCTCT	1080
CTAAGGAGGG	TATCTGTCT	CCCCAGCGGC	TGGATGGGGC	TGGCACCCAG	CCTGGCAGG	1140
AGGCCACTGG	CAACCTGTC	CTACATCACT	GGCCCTCGCA	GGAGCCGC	CCTGGCTCCC	1200
TGGGGCAGCC	CCATCTGAA	GCTCTGGAT	TCCCGCTGGA	GCTGAGGGAG	TCGCAGCTAC	1260
TGCGCTGATGG	GGAGAGACTA	GCACCCAATG	GGCGGGAGCG	AGAGGCTCT	GCCATGGGCA	1320
GGCAGGGAGGG	CATGAGGGC	GTGAGCACAG	GGGACTGTGG	GGAGGTGCTA	CGGGGGCGGAG	1380
TGATCCAGAG	CACGCCAGCG	AGGCCAGGG	CATCCCAGGA	GGCCAATTG	CTGACCCCTGG	1440
CCCAGAAGGC	TGTGGAGCTG	GGCTCACTGC	AGAATGAAA	GGATGGCAGT	GGTCTGTAA	1500
AGAACGGGAA	AAAGTGTATTG	GCCTCAACTA	CCAAGTGTGG	GGTGGAGTT	TCTGAGCCTT	1560
CCTTAGCCAC	CAAGCGAGCA	CGAGAAGACA	GTGGGATGGT	ACCCCTCATC	ATCCCACTGT	1620
CTGTGGCTGT	GCAGAACCTGT	GACCCAACTG	AGGCAGGCCA	GGCTGGAGGT	CTTGATGAGG	1680
ACGGGAAGGG	TCTTGAACAG	AACCCCTGTC	AGCACAAGGC	ATCAGTCATC	GTCAACCCGCA	1740
GGCGGTCCAC	CCGAATCCCC	GGGACAGATG	CTCAAGCTCA	GGCGGAGGAC	ATGAATGTCA	1800
AGTTGGAGGG	GGAGCCTTCC	GTGCGGAAAC	CAAAGCAGCG	GGCCAGGCC	GAGCCCCCTCA	1860
TCATCCCCAC	CAAGGGGGC	ACTTTCATCG	CCCCCTCCGT	CTACTCCAA	ATCACCCCAT	1920
ACCAGAGCCA	CCTGCGCTCT	CCCCGTGCC	TAGCTGACCA	CCCCCTCTGAG	CGGAGCTTTG	1980
AGCTACCTCC	CTACACGCCG	CCCCCCATCC	TCAGCCCTGT	GGGGGAAGGC	TCTGGCTCT	2040

ACTTCAATGC	CATCATATCA	ACCAGCACCA	TCCCTGCC	TCCCTCCATC	ACGCCTAAGA	2100
GTGCCCATCG	CACCGCTGCTC	CGGACTAAC	GTGCTGAAGT	AAACCCGGCT	GTCCCTCTG	2160
TGATGGGGGA	GGCCACCCCA	GTGAGCATCG	AGCCACGGAT	CAACGTGGC	TCCCAGTCC	2220
AGGAGAAAAT	CCCCTTGATG	AGGAGCCGTG	CCCTGGCAGC	TGAGATCCC	CACAAGGCTG	2280
ACTTGGTGTG	GCAGCCATGG	GAGGACCTAG	AGAGCAGCG	GGAGAAGCAG	AGGCAAGTGG	2340
AAGACCTGCT	GACACCGGCC	TGCTCCAGCA	TTTCCCTGG	TGCTGGCACC	AACCAGGAGC	2400
TGGCCCTGCA	CTGTCGAC	GAATCCAGAG	GAGACATCTC	CGAAACGCTG	AATAAGCTG	2460
TGCTGAAGAA	GCCCCGCG	CCCCACAACC	ATCCGCTGGC	AACTTATCAC	TACACAGGCT	2520
CTGACCAAGTG	GAAGATGGCC	GAGAGGAAGC	TGTTCAACAA	AGGCATTGCC	ATCTACAAAGA	2580
AGGATTCTT	CCTGGTGCAG	AAAGCTGATCC	AGACCAAGAC	CGTGGCCAG	TGCGTGGAGT	2640
TCTACTACAC	CTACAAAGAAG	CAGGTGAAAA	TCGGCCGCAA	TGGGACTCTA	ACCTTTGGGG	2700
ATGTGGATAC	GAGGCGATG	AAGTCGGGAG	AGGAAGAGGT	TGAAGTGGAT	ATTAAGACTT	2760
CCAAAAGTT	CCCCAAGGTG	CCTCTTCCCA	GAAGAGAGTC	CCCAAGTGA	GAGAGGCTGG	2820
AGCCCAAGAG	GGAGGTGAAG	GAGGGCAGGA	AGGAGGGGA	GGAGGAGGTG	CCAGAGATCC	2880
AAGAGAAGGA	GGAGCAGGAA	GAGGGGCGAG	AGCGCAGCG	CGGGCAGCG	GCAGTCAAAG	2940
CCACGCAGAC	ACTACAGGCC	AATGAGTCGG	CCAGTGCAT	CCTCATCC	CGGAGCCACG	3000
AGTCCAACGC	CCCTGGGTCT	GCCGGTGGCC	AGGCCTCGGA	GAAGCCAAGG	GAAGGGACAG	3060
GGAAGTCACG	AAGGGCACTA	CCTTTTCAG	AAAAAAAAAA	AAAAAAACAA	AAAGCTT	3117

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAATTCCGCA	CGAGGTCACT	TTCTGTGGA	ACACAGAGGC	TGCGTGTCCC	ATTCAGACAA	60
CGACGGATAC	AGACCAAGGC	TGCTCTATAA	GGGATCCAA	CACTGGATT	GTGTTAAC	120
TTAATCCGCT	AAACAGTTG	CAAGGTATATA	ACGTCTCTGG	CATTGGGAAG	ATTTTATGT	180
TTAATGTCG	CGGCCACAATG	CCTGTCGTC	GGACCATCCT	GGGAAACCT	GCTTCTGGCT	240
GTGAGGCGA	AACCCAAACT	GAAGAGCTCA	AGAATTGGA	GCCAGCAAGG	CCAGTCGAA	300
TTGAGAAAAG	CCTCCAGCTG	TCCACAGAGG	GCTTCATCAC	TGTCACCTAC	AAAGGGCCTC	360
TCTCTGCCAA	AGGTACCGCT	GATGCTTTA	TGTCGGCTT	TGTTGCAAT	GATGATGTTT	420
ACTCAGGCC	CCTCAAAATC	CTGCATCAAG	ATATCGACTC	TGGCGAAGGG	ATCCGAAACA	480
CTTACTTGA	GTTGAAACC	GCCTTGGCCT	GTGTTCTTC	TCCAGTGGAC	TGCCAAGTCA	540
CCGACCTGGC	TGGAATGAG	TACGACCTGA	CTGGCCTAA	CACAGTCAGG	AAACCTTGG	600
CCGCTGTTG	CACCTCTGTC	GATGGGAGAA	AGAGGACTTT	CTATTTGAGC	GTTTGCAATC	660
CTCTCCCTTA	CATTCTGGG	TGCCAGGGCA	GGCGAGTGGG	GCTTGTCTTA	GTGTCAGAAG	720
GCAATAGCTG	GAATCTGGGT	GTGGTGCAGA	TGAGTCCCCA	AGCCGCGCCG	ATAGGATCTT	780
TGAGCATCAT	GTATGCAAC	GGTACAAGT	GTGGGAACCA	GCGCTTCTCC	ACCAGGATCA	840
CGTTTGTAGT	TGCTCAGATA	TCGGGCTCAC	CAGCATTCA	GTCTCAGGAT	GTTGTGAGT	900
ACGTGTTAT	CTGGAAACT	GTGGAACCT	GTCGGCTGT	CAGAGTGGAA	GGGGACAAC	960
GTGAGGTAAGA	GAACCCAAAGG	CATGGCAACT	TGATGACCT	GAAGGCCCCG	GGCCTCAACG	1020
ACACCATCGT	GAGCGCTGGC	GAATACACTT	ATTACTTGG	GGTCTGTGGG	AACTTTCTC	1080
CAGACGCTG	CCCCACAAGT	GACAAGTCCA	AGGTGGTCTC	CTCATGTCAG	AAAAAGCGGG	1140
AACCCGAGGG	ATTCACAAA	GTGGCAGGT	TCCCTGACTCA	GAAGCTAAC	TATGAAAATG	1200
GCTTGTAA	AATGAACCT	ACGGGGGGGG	ACACTTGC	TAAGGTTTAT	CAGCGCTCCA	1260
CAGCCATCTT	CTTCTACTGT	GACCCGGGCA	CCCAGCGGGC	AGTATTTCTA	AAGGAGACTT	1320
CAGATTGTT	CTACTTGT	GAGTGGGAA	CCCGAGTATG	CTGCCACCT	TTCGATCTGA	1380
CTGAATGTT	ATTCACAAAGT	GGGGCTGGCA	ACTCTTCGA	CCTCTCGTCC	CTGTCAGGT	1440
ACAGTGACAA	CTGGGAAGCC	ATCACTGGG	CGGGGGACCC	GGAGCACTAC	CTCATCAATG	1500
TCTGCAAGTC	TCTGCCCTG	CAGGCTGGCA	CTGAGCGCTG	CCCTCCAGAA	GCAGCCGGCT	1560
GTCTGCTGG	TGGCTCAAAG	CCCGTGAAC	TGGCGAGGGC	AAGGGAGCGA	CCTCAGTGG	1620
GAGATGGCAT	AATTGCTCTG	AAATACGTTG	ATGGCGACTT	ATGTCAGAT	GGGATTGCGA	1680
AAAAGTCAC	CACCATCCGA	TTCACCTGCA	GCGAGAGCCA	AGTGAACCTC	AGGCCCATGT	1740
TCATCAACG	CGTGGAGGAC	TGTGAGTACA	CCTTGTGCTG	GCCCCACAGCC	ACAGCCTGTC	1800
CCATGAAGAG	CAACGAGCAT	GATGACTGAC	AGGTCAACAA	CCCAAGCACA	GGACACCTGT	1860
TTGATCTGAG	CTCCCTAAAGT	GGCAGGGCGG	GATTCAACAG	TGCTTACAGC	GAGAAGGGGT	1920
TGGTTACAT	GAGCATCTGT	GGGGGAGAATG	AAAAGTCCC	TCTTGGCTG	GGGGCCTGCT	1980
TTGGACAGAC	CAGGATTAGC	GTGGGCAAGG	CCAACAAGAG	GCTGAGATAC	GTGGACCAAG	2040
TCCTGCACTG	GGTGTACAAG	GATGGGGTCC	CTTGTCCCTC	CAAATCCGC	CTGAGCTATA	2100
AGAGTGTGAT	CAGTTCTG	TGCAAGGCC	AGGCGGGGCC	AACCAATAGG	CCCATGCTCA	2160
TCTCTCTGGA	CAAGCAGACA	TGCACTCTC	TCTTCTCTG	GCACACGCC	CTGGCCTGG	2220
AGCAACGAC	CGAATGTTCC	GTGAGGAATG	GAAGCTAT	TGTTGACTTG	TCTCCCCCTTA	2280
TTCATCGCAC	TGGTGGTTAT	GAGGCTTATG	ATGAGAGTGA	GGATGATGCC	TCCGATACCA	2340
ACCCGTGATT	CTACATCAAT	ATTGTCAGC	CACTAAATCC	CATGCACCGA	GTGCCCTGTC	2400
CTGCCGGAGC	CGCTGTGTGC	AAAGTTCTA	TTGATGGCC	CCCCATAGAT	ATCGGCCGGG	2460
TAGCAGGAC	ACCAATACTC	AATCCAATAG	CAAATGAGAT	TACTTGAAT	TTTGAAGCA	2520

GTACTCCCTG	CCAGGAAATT	AGTTGTAAT	AAAATTGAAC	CTGCTCAACA	GCTGAGGGAG	2580
ACTAGAAATG	ATGGGTCCAT	ATCCTGGTGC	ATTGTCATAC	AATTCAAACA	ATGGTGCAGC	2640
TACCAAGCTT	TAATTTTGTAG	GGACTGAAA	CAAGGCTTT	TCTTGAAGCT	GAACCAGAAA	2700
CAACCTCTTA	TGTTCTTAG	GCTTGTAAAT	ATGTCAGGA	ATATATGGAT	ACTGAGGAGG	2760
TTCAAAATT	GGTCTCCACC	AGTTACCAAT	GCAATCGTC	ATGACCCAGT	CTTGCAAAAC	2820
TCCATCCCTG	CGACCCAGTA	TCTCTGTCT	TAAGCGTTT	AGTCCTCAA	CTTCATCTTC	2880
TCCTGGGTTA	AGTTACCCAC	CAGGTAGTT	GAAGAAAGT	GTTCCAGCT	GCACCGAGTAA	2940
CACATGGGGT	AGCCGGTGCT	CATGTACAAAT	CAGAACCCCT	TCTACAGTCC	TCCTCATTC	3000
AATTATCA	AATTCTTCCC	TCTATGCCCTG	AAATCTGGCT	GCAACAGAGC	TGTCCTTCTC	3060
GTAGAGGGGC	TCTTTTGTAC	CAAAGTATA	ATTGGTAAGA	GGGTACAGGT	TGATGGTGG	3120
CTCCAGGGTG	AGGGGCTTCG	TCTGCTGGAT	GTACTTGTG	CCGAACGTGAG	TGACCCCCCG	3180
GGGCCAGCCG	GTCTGGAGC	GATTGGCCGG	TACACAGAC	ATGCTGGCGA	GCTCCGGCGC	3240
TGACGGCGAG	CAGAAAGTGG	CAGGCAGGGT	AGACTTTCCC	CGTGGGGAA	GCCTCGTGCC	3300
GAATTC						3306

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAATTCCGCA	CGAGAATGGA	TCAACCTCAA	CAACACGTTA	AAGCTAGACG	AAAGAAGTAA	60
TACACAGTGT	ATGAGCTCA	CATGAAATAC	CCGGATGTAA	ATCCAAAGAA	ACAGGAAGCA	120
GATTGGGGT	TGCCACGGAC	AAGGGCGGTG	GGAGGAGAAA	ATGGAGAGTA	ACGGGACTTT	180
ACTTTGGAG	TGATGAGAAT	GTTTGGAGC	TAGATAGAAG	TGGTGGTTGT	ACACCATTGT	240
GGATGTACTA	CCACTTAATT	GTTCACTTAA	AAAGTTAATT	TATGTGAATT	GCATCTTAAT	300
TAAAAAACAG	GATAAACATTC	CAACTCCTGG	ACATTATCCT	TCCTTCCAT	TTGATGTCA	360
GCCCGTGT	GAATTCTCAT	CGGGTTGGT	CACTGCACTT	AAAGATGTGGA	GAAATTAGGA	420
CGCACAGGT	AGAGGAAGGA	TAACACTGAT	TAAGGTAGTG	CTTTCTAGG	TTTCCCCTAA	480
ACAATTAAAC	AGATGGATAG	TGGCACCACT	TACCGAGATGG	AAAACCAGC	GGAAAGGAAGA	540
TTTGGGGGAG	AAGTTAAGTT	TGTCTTGGC	CTGTGTTTG	CAACCTGAGT	GTAAAAGACA	600
TATGTTAAGT	CTTCAGTGGC	GAAACACTAA	AACTAGAAAT	GGATCAGAAAT	TTTATCTTTG	660
GATGTGACTT	CTCAAGGATG	GTCTTGTCA	TTCACTGCT	GTCAAATGA	CAAGATGGGC	720
AATCTTTCC	TGAAGGTCCA	AGCACCTGAA	CGTGGCAGGG	TGACCCGATT	CCGATTGCT	780
TAGAACAAATC	CTAGTTCATG	CCTATTGTCC	CTCATGTAAT	TAATATCACT	CTCAAAATGT	840
CTCATTGTTG	GCAAAATATT	CTGCAACGTG	ATGGCGCAGC	TCTCGCGGCC	CGAGCGGCC	900
GACCTTGTCT	TCGAGGAAGA	GGCACCTCCC	TATGAGGGAGG	AAATCATCGG	GAACCAATT	960
TCTGCAAT	GCTGGCTCA	TCATACGAG	TTCAACACGG	GCCCCCGGAA	GCCCCAGGCTC	1020
AATCAGCTAT	ACGAGCGG	ACTCAAGCTG	CTGCCCTGCA	GCTACAAACT	CTGGTACCGA	1080
TACCTGAAGG	CGCGTCGGG	ACAGGTGAAG	CATCGCTGTG	TGACCGACCC	TGCTCTGTGG	1140
GATGTCAACA	ACTGTCTATG	GAGGGCCTT	GTGTTCATGC	ACAAGATGCC	TCGCTCTGTGG	1200
CTAGATTACT	GCCAGTCTC	CATGACCG	GGCGCGCTGA	CACACACCCG	CCGCACCTTC	1260
GACCGTGGCCC	TCCGGGCACT	CCCCATCACG	CAGCACTCTC	GAATTGGCC	CCTGTATCTG	1320
CGCTTCTGC	GCTCACACCC	ACTGCCCTGAG	ACAGCTGTG	GAGGCTATCG	GGCCTTCTC	1380
AAGCTGAGTC	CTGAGAGTGC	AGAGGAGTAC	ATTGAGTACC	TCAAGTCAAG	TGACCGCTG	1440
GATGAGGGCG	CCCAGCCGCT	GGCCACCGTG	GTAAACGAGC	AGCGTTCTG	GTCTAAGGCC	1500
GGCAAGTCCA	ACTACCAGT	GTGGCACG	CTGTGCGACC	TCTATCTCCA	GAATCCGGAC	1560
AAGGTACAGT	CCCTCAATGT	CGACGCCATC	ATCCGGGGG	GGCTCACCCG	CTTCACCGAC	1620
CAGCTGGCA	AGCTCTGGT	TTCTCTGCC	GACTACTACA	TCCGCAGCGG	CCATTTCGAG	1680
AAGGCTCGGG	ACGTGTACGA	GGAGGCCATC	CGGACAGTGA	TGACCGTGCG	GGACTTCACA	1740
CAGGTGTTTG	ACAGCTACGC	CCAGTCCAG	GAGAGCATGA	TGCTGTGCAA	GATGGAGACC	1800
GCCTCGGAGC	TGGGGCGCGA	GGGAGGAGAT	GATGTGGC	TGGAGCTGCC	CCTGGCCCGC	1860
TTGAGACGC	TCATCGAC	CGGGCCCTG	CTCTCAAC	GGCTCTTGT	GGCCAAAAAC	1920
CCACACCAAG	TGCACCGAGT	GCACAAAGCT	GTGCCCTCTG	ACCGAGGCCG	CCCCGGGAG	1980
ATCATCAACA	CCTACACAGA	GGCTGTGCG	ACGGTGGACC	CCTTCAGGC	CACAGGCAAG	2040
CCCCACACTC	TGTGGGTGGC	GTTTGCCAAG	TTTATGAGG	ACAAACGGACA	GCTGGACGAT	2100
GCCCCGTGTCA	TCCTGGAGAA	GGCCACCAAG	GTGAACCTCA	ACGAGGTGGA	TGACCTGGCA	2160
AGCGTGTGGT	GTCAGTGGG	AGAGCTGGAG	CTCCGACACG	AGAACTACGA	TGAGGCC	2220
CGGCTGCTG	GAAGGCCAC	GGCGCTGCC	GGCCGCCGGG	CCGAGTACTT	TGATGGTCA	2280
GAGCCCGTGC	GAACCCGCT	GTACAAGTC	CTGAAGGTCT	GGTCCATGCT	CGCCGACCTG	2340
GAGGAGAGCC	TCGGCACCTT	CCAGTCCACC	AAAGCCCGTGT	ACGACCGCAT	CCTGGACCTG	2400
CGTATCGCAA	CACCCAGAT	CGTCATCAAC	TATGCCATGT	TCTTGGAGGA	GCACAAGTAC	2460
TTCGAGGAGA	GCTTCAAGGC	TCAGGACGCC	GGCATCTCGC	TGTTCAAGTG	GCCCAACGTG	2520
TCCGACATCT	GGAGCACCTA	CCTGACCAAA	TTTATTGCC	GGCTATGGGG	CCGCAAGCTG	2580
GAGCGGGCAC	GGGACCTGTT	TGAACAGGCT	CTGGACGGCT	GGCCCCC	ATATGCCAAG	2640
ACCTTGTAAC	TGCTGTACGC	ACAGCTGGAG	GAGGAGTGGG	GGCTGGCCCG	GCAATGCCATG	2700
GCCGTGTA	AGCGTGCAC	CAGGGCCGTG	GAGCCCGCCC	AGCAGTATGA	CATGTTCAAC	2760

ATCTACATCA	AGCGGGCGGC	CGAGATCTAT	GGGGTCACCC	ACACCCGCGG	CATCTACCAG	2820
AAGGCCATTG	AGGTGCTGTC	GGACGAGCAC	GCGCGTGAGA	TGTGCTGCG	GTTTGCAGAC	2880
ATGGAGTCA	AGCTCGGGGA	GATTGACCGC	GCCCGGGCCA	TCTACAGCTT	CTGCTCCCAG	2940
ATCTGTGACC	CCCGGACAC	CGGGCGCTTC	TGGCAGACGT	GGAAGGACTT	TGAGGTCGG	3000
CATGGCAATG	AGGACACCAT	CAAGGAAATG	CTGCGTATCC	GGGCCAGCGT	GCAGGCCACG	3060
TACAACACGC	AGGTCAACTT	CATGGCCTCG	CACATGCTCA	AGGTCTCGG	CAGTGCCACG	3120
GCCACCGTGT	CTGACCTGGC	CCCTGGGAG	AGTGGCATGG	ACGACATGAA	GCTGCTGGAA	3180
CAGCAGGAG	AGCAGCTGGC	GGCTGAGGCG	GAGCGTGACC	AGCCCTTGCG	CGCCAGAGC	3240
AAGATCTGT	TCTGTGAGGAG	TGACGCCCTC	CGGGAGGAGC	TGGCAGAGCT	GGCACAGCAG	3300
GTCAACCCCG	AGGAGATCCA	GCTGGCGAG	GACGGAGGAGC	AGGACGAGAT	GGACCTGGAG	3360
CCCAACGAGG	TTCGGCTGGA	GCACGAGAGC	GTGCCAGCGC	CAGTGTGTTG	GAGCCTGAAG	3420
GAAGACTGAC	CCGTCCTCTC	GTGCGAATT	CGGCACGAGC	AAGACCAAGCC	CCCAGATCAT	3480
TTGCCCTAA	GGTTTCCCT	CGAATCACA	AATGTTTCAA	GGAATCTCAA	ATTTTACAAA	3540
GTGTTGAATG	TGGCATTGG	TGGCCTGTGG	TCTGTCCTC	TCTCTGTAGC	TGTTTCTCC	3600
CTACATCCTT	GAAAGGAAGT	TGACGCTGCT	CCCTCCATCCG	CAGACCTCCC	TTTCCAGCGC	3660
CCAGGGCATG	GGGTGCTGTG	AGGGCAGCAT	GCTAGGTGTC	ACCGTGTCTC	TGGCCTCCAG	3720
GCCCCTGTC	CTCTGTCCTC	TAGGCCACTA	AGGCCCTGGC	CCATTGTGC	TAAACAGGCA	3780
GTCGGACCTA	GAAAGAGCAG	ACAATCTCTC	TGGGTACCAA	GTCTGGCTAG	GAGCTGGTCT	3840
CCTGACTGGG	ATCCAGGCT	TCTCCCTCTC	CCATGTGAAT	TCCCAGGGGC	AGAGCCTGAA	3900
ATGTTGAACA	CAGCACTGGC	CAAAGAGATG	TCACCGTGGG	AACCGAGGCT	CTCTTCTCT	3960
CCTGCTGCT	TTCTGGGTT	CAGAGTAGCT	GAGGCTTGTC	TGAGAGGAGT	TGGAGTGCTG	4020
GTGTTCAACC	TGGTTGGTGT	GCTTGTCTT	GAGGGCACTT	AGAAAGCCCA	GCCCAAGCCCT	4080
TGCTCTGCC	CTGCAACACAG	CGGAGCAGCT	TTTCTAGGTA	TGCTCTTGAT	TTCTGCAGAA	4140
GCAGCAGGTG	GCATGGAGGC	AAGAGGAAGT	GTGACTGAAA	CTGTCACACT	ATAGCCGGC	4200
TGCCGTATTG	AGAGGGCT					4218

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAGCTCGGGC	GCCTCGGAGT	CGACACTAGT	GGATCCAAAG	AATTGGCAC	GAGGGAAACT	60
CAACGGGTGA	CGAGTGGAGG	ACAGGGACAG	AGGCCCTCTGT	GGTGGAACGA	CCCCACCTCG	120
AGGAGCTTCC	TGAGCAGGTG	GCAGAAAGATG	CGATTGACTG	GGGGCAGCTT	GGGGTAGAGG	180
CACTGCTCTA	GGGGACTGAC	TCTGGCATCT	CTGCGGAGGC	TGCTGGAATC	GACTGGGCA	240
TCTTCCCGGA	ATCAGATTC	AAGGATCTG	TGGGTGATGG	GATAGACTGG	GGAGACGATG	300
CTGTTGCTT	GCAGATCACA	GTGCTGGAG	CAGGAACCCA	GGCTCCAGAA	GGTGTGCCA	360
GGGGCCAGA	TGCCCCGACA	CTGCTGAAAT	ACACTGAGAC	CCGGAAATCAG	TTCCCTGATG	420
AGCTCATGGA	GCTTGGAGTC	TTCTTAGCCC	AGAGAGCAGT	GGAGTTGAGT	GAGGAGGAG	480
ATGTCCTGTC	TGTGAGCCAG	TTCCAGCTGG	CTCCAGCCAT	CCTGAGGGC	CAGACCAAAG	540
AGAAGATGGT	TACCATGGTG	TCAGTGCTGG	AGGATCTGAT	TGGCAAGCTT	ACCACTCTC	600
AGCTGCAACA	CCTGTTATG	ATCTGGCCT	CCACCAAGGT	TGTGGACCGA	GTGACTGAAT	660
TCCCTCAGCA	AAAGCTGAAG	CAGTCCCGAGC	TGCTGGCTTT	GAAGAAAGAG	CTGATGGTGC	720
AGAAGCAGCA	GGAGGCACTT	GAGGAGCAGG	CGGCTCTGGA	GCCTAAAGCTG	GACCTGCTAC	780
TGGAGAAGAC	CAAGGAGCTG	CAGAAAGCTG	TTGAAGCTGA	CATCTCCAAG	AGGTACAGCG	840
GGCGCCCTGT	GAACCTGTG	GGAACTCTC	TGTGACACCC	TCCGTGTTCT	TGCCCTGCCCA	900
TCTTCTCCG	TTTGGGATG	AAGATGATAG	CCAGGGCTGT	TGTTTGGGG	CCCTCAAGG	960
CAAAAGACCA	GGCTGACTGG	AAAGATGAAA	GCCACAGGAA	GGAAGGGCA	CCTGATGGTG	1020
ATCTTGGCAC	TCTCCATGTT	CTCTACAAAGA	AGCTGTTG	ATTGGCCCTG	TGGTCTATCA	1080
GGCGAAAACC	ACAGATTCTC	CTTCTAGTTA	GTATACCGCA	AAAAGCTTCT	CGAGAGTACT	1140
TCTAGAGCGG	CCGGGGGCC	ATCGATTTTC	CACCCGGGTG	GGGTAC		1187

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCCTCACTAA	AGGAAACAAA	AGCTGGAGCT	CGCGCGCTG	CAGGTGACCA	CTAGTGGATC	60
GAAAGTTCTG	TACGCCAAGC	TCGAAATTAA	CTCTGGCTG	ACCCATAAAC	ATTGTCTGA	120

TCTAGGATAT	AGTTGCGTTT	CTTGCAGGCA	GCAATCTGGA	TGAGGCAGGT	GAGGCAGTGG	180
GTGGCCTGCT	GGATCAGGAC	ATCCCAGCGG	CCAGCATAGT	TCCGCTGCCG	GCGTAGGCC	240
ATACCCCGA	TCTTATCCAT	GATGGCATTG	GTACCCAGGA	TGTTGTACTT	CTTGGAAAGGG	300
TTGGAGGCTG	CATGTTGAT	GGCCCATGTG	GTCTTGCAG	CAGCAGGCAAG	GCCCACCATC	360
ATCAGAATCT	CACATTCTGC	CTTGTCTTT	GGTCAACAGG	TGCCCCGGAT	ACGCTCACTA	420
AGGGGAAAGT	GCTGGATGAA	GGTAACACCC	GGGAGGACAG	AACACTAGGG	CTCTGTCTC	480
TGTCCGAAGT	TGAACCTCCAC	TGGCAATTG	TTACCCAGGA	CATGAGGATA	GAGGGCCTGA	540
CCCCCGAAGG	CTTCTCTCTG	GATTGGAAA	GCAATGCCCA	TCCACTTCC	ATTCTTGGTA	600
AAAGACATTG	CCACGTCATT	TCCACATTCA	AAATCCGCAA	AGCAGGCAAT	CACCGGAGAG	660
CTCTGGGTG	CTAGGAGAGC	GGCTGGGCC	GCAGACTGGG	GGGAAAGCTC	CGCAGCGCA	720
GTGGGCCCA	GGATCAGGCC	CCCGTGGCC	TGAGAAGGCC	CAGTCTGGC	TGGAGCGGGA	780
GCTGGACAGT	GTGGCCTTGC	TTCCGCCCCC	GGGAGCGCTG	CGAGTGTGCG	GGCCTCGGGT	840
GGATTGGCTG	AGCACCAATA	CCTCACGGT	GCAACCTGG	GGTTTTAGCT	CCCTTGGTTT	900
TAATCCCTA	GGGGGGGGTG	GGGGCACGGG	AGGAAGGATE	GGCCAGCTGG	GTGCAATCCT	960
GCTGTAAGCC	AGCCATTCTT	TGATTTCTTA	GAATTAACCA	AACGTCGCG	CCGGAGGCCG	1020
CGGGGGCCCG	AGCGGAGCAG	CCCGGCTGA	GGTCCCGAG	TCGGCCGCTC	GGGGCTGCGC	1080
TCCGCCCCG	GGACCCCGGC	CTCTGGCCGC	GCCGGCTCCG	GCCTCCGGGG	GGGCCGGGGC	1140
CGCCGGGACA	TGGTGGCAGT	CGCACCCCTT	CCCCCGCCGC	GCTGAGCTCG	CCGGCCGGCGC	1200
CCGGGCTGG	ACGTCGAGC	GGGAAGATGT	TTCGGCCCT	GAAGAAGCTG	GTGGGGTGC	1260
ACGAGCCCCC	GGGGGGGGAC	AAGAACATCC	CCGGGGGGCT	GCAGTCATG	AACCAGGCGT	1320
TGCAGAGGCC	CTTCGCCAAG	GGGGTGCAGT	ACAACATGAA	GATAGTGTAC	CGGGGAGACA	1380
GGAACACGGG	CAAGACAGCG	CTGTGGCACC	GCTGCAAGGG	CCGGCGTTC	GTGGAGGAGT	1440
ACATCCCAAC	ACAGGAGATC	CAGTCACCA	GCATCCACTG	GAGCTACAAG	ACCACGGATG	1500
ACATCGTAA	GGTTGAAAGTC	TGGGATGTAG	TGACAAAGG	AAAATGCAA	AAGCGAGGCC	1560
ACGGCTTAA	GATGGAGAAC	GACCCCGAG	AGNCGGAGTC	TGAAATGGCC	CTGGATGCTG	1620
AGTTCTGGA	CGTGTACAAAG	AACTGCAACG	GGGTTGGTCAT	GATGTCGAC	ATTACAAGC	1680
AGTGGACCTT	CAATTACATT	CTCCGGGAGC	TTCCAAAAGT	GCCCACCCAC	GTGCCAGTGT	1740
GCGTGTCTGG	GAACATACCGG	GACATGGGGC	AGACCCGAGT	CATCTGCGC	GACGACGTGC	1800
GTGACTTCAT	CGACAACTC	GACAGACCTC	CGGTTCTC	CTACTTCCGC	TATGCTGAGT	1860
CTTCATGAA	GAACAGCTTC	GGCCCTAAAGT	ACCTTCATAA	GTTCCTCAAT	ATCCCATTTT	1920
TGCAGCTTC	GAGGGAGACG	CTGTTGCGC	AGCTGGAGAC	GAACAGCTG	GACATGGACG	1980
CCACGCTTGA	GGAGCTGTG	GTGAGCAGG	AGACGGAGGA	CCAGAACTAC	GGCATCTTCC	2040
TGGAGATGAT	GGAGGCTGCC	AGCCGTGGCC	ATCGGTCCCC	ACTGGCGGCC	AACGGGCAGA	2100
GCCCATCCCC	GGGCTCCCG	TCACCACTC	TGCTTCGACC	CGCTGTGTC	ACGGGGAGCT	2160
CCAGCCCCG	CACACCCCG	CCCCCCCCAC	AGCTGGCCCT	CAATGTCGC	CCACCATCCT	2220
CTGTGCCCCC	TGTACCAACC	TCAGAGGCC	TGCCCCCACC	TGCGTGC	TCAGCCCCG	2280
CCCCACGGCG	CAGCATCATC	TCTAGGCTGT	TTGGGACGTC	ACCTGCCACC	GAGGCAGGCC	2340
CTCCACCTCC	AGAGCCAGTC	CCGGCGCAC	AGGGCCAGC	AACGTCAG	AGTGTGGAGG	2400
ACTTGTCCC	TGACGACGGC	CTGGACCGCA	GTTCCTGGA	AGACACAA	CCCGCCAGGG	2460
ACGAGAAGAA	GGTGGGGGCC	AAGGCTGCC	AGCAGGACAG	TGACAGTGT	GGGGAGGCC	2520
TGGGCAGCAA	CCCGATGGTG	GCAGGGTTC	AGGACGATGT	GGACCTCGAA	GACCAACAC	2580
GTGGGAGTCC	CCCGCTGCTC	GCAGGCCCTG	TCCCCAGTC	AGACATCACT	CTTTCGAGTG	2640
AGGAGGAAGC	AGAACATGGCA	GCTCCCACAA	AAAGCCCTGC	CCCAGCTCCC	CAGCACTGCT	2700
CAGAGCCAGA	GACCAAGTGG	TCTCCATAC	CGCTTCGAA	GCCACGGAGG	GGGACAGCTC	2760
CCACGAGGC	CGCAGCACCC	CCCTGGCCAG	CGGGTGTCTC	TGTCGCACA	GGTCCGGAGA	2820
AGCGCAGCAG	CACCAAGGCC	CCTGCTGAGA	TGAGGCCGG	GAAGGGTGAG	CAGGCTCTC	2880
CGTCGGAGAG	TGACCCGAG	GGACCCATTG	CTGCACAAAT	GCTGCCCTC	GTATGGATG	2940
ACCCCGACTT	TGAGAGCGAC	GGATCAGACA	CACAGCGCAG	GGCGGATGAC	TTTCCCGTGC	3000
GAGATGACCC	CTCCGATGTG	ACTGACGAGG	ATGAGGGCCC	TGCGGAGGCC	CCCCCACCCC	3060
CCAAAGCTCC	TCTCCCCGCC	TCTCAACTG	AGAATGACTG	GGACCTCTC	GGGCTGGGGC	3120
TGGAGGAGGC	CGGACCCAAG	GAGAGCAGTG	AGGAAGGTA	GGAGGGCAA	ACCCCTCTA	3180
AGGAGAAGAA	AAAAAAACAA	AAAAGCTTCT	CGAGAGTACT	TCTAGAGCGG	CCGCAGGGCCC	3240
ATCGATTTC	CACCCGGGTG	GGTACCAAGG	TAATGTCACC	CAATTGCGCC	TATAGTGAGT	3300
CGTATT						3306

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGCAGGGGCCA GAGTGGGCTG

20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCAGTCCTGG CCTGCCGGATG

20

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTCGACAGGA GAATTGGTTC

20

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCCTGGGTTG GGTGCGGGAC

20

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TGGTCGGGTG TTTGTGAGTG

20

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCTCTTCGGT CTCCCTCAGTG

20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGATTGCTAG TCTCACAGAC

20

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTAAGGGTGG CTGAAGGGAC

20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ACCTTCCTC CCTGTACAG

20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGGTCGGGTG TTTGTGAGTG

20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ACACCATTCC AGAAATTTCAG

20

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AAACTGCAGG TGGCTGAGTC

20

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTCCTAATGT TTTCAAGGGAG

20

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AAAACCTATG GTTACAATTG

20

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TCCTAGACAT GGTTCAAGTG

20

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GATATAATTA GTTCTCCATC

20

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGCCTGTTC CAGGCTGCAC

20

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGACGGCGAC CTCCACCCAC

20

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGGCTCCTCC GACGCCCTGAG

20

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AGTCTAGCCC TGGCCTTGAC

20

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTCACTGGGG ACTCCGGCAG

20

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CAGCTTCCCC TGGGCACATG

20

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CACAGCTGTC TCAAGCCAG

20

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ACTGTTCCCC CTACATGATG

20

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATCATATCCT CTTGCTGGTC

20

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GTTCCCAGAG CTTGTCTGTG

20

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTTTGGCAGA CTCATAGTTG

20

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TAGCAGGGAG CCATGACCTG

20

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CTTGGCCCA GAAGCGAGAG

20

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCTCTCTCTC TCTCTCTCTC

20

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TCCCCGGTGA TTCCGGCCAAG

20

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTTTTGAAAT TCGGCACGAG

20

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CCCCCTGGTCC GCACCAAGTTC

20

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GAGAAGGGTC GGGGCGGCAG

20

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AAATCACATC GCGTCAACAC

20

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TAAGAGAGTC ATAGTTACTC

20

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GCTCTAGAAG TACTCTCGAG

20

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ACTCTGGCCA TCAGGAGATC

20

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CAGGCCGTGT AGATGTTCTG

20

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AGTGGCAGGC AGAAGTAATG

20

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGTTGGAGAA CTGGATGTAG

20

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CTATTCAGAT GCAACGCCAG

20

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CCATGGCACA CAGAGCAGAC

20

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GCTACCATGC AGAGACACAG

20

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CAGGCTGACA AGAAAATCAG

20

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGCACCGATA GAGGAGAGAC

20

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TGGGTGATGC CTTTGCTGAC

20

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

AAAACAAGAT CAAGGTGATG

20

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TTGCCACAT TGCTATGGTG

20

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GACCAAGATC AGAAGTAGAG

20

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CCCCCTGGGCC AATGATGTTG

20

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TCTTCCCCACC ATAGCAATG

19

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TGGTCTTGGT GACCAATGTG

20

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACACCTCGGT GACCCCTGTG

20

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TCTCCAAGTT CGGCACAGTG

20

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ACATGGGCTG CACTCACGAC

20

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GATCCTCTGA ACCTGCAGAG

20

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GGAAATGAGG TGGGGCGATC

20

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CTTGCCTTG GACAAGGATG

20

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GCACCTGCCA TTGGGGGTAG

20

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GGTGAAGCC ATTGACGGTG

20

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TGCGTCTCTC GTCGCTGCTG

20

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GCGGAAACTC TGTGGTGCTG

20

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

AGGATTGCCT TCCTCTACTG

20

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

TGTCTGTTTC ACCAGGGCAG

20

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

CCAGTGCCTC TATGCATGTC

20

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

AGGAAGCCCA CGCACACCCAC

20

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CCCTTTGTTTC CCTGATCTTC

20

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CGCTCGGGAT CCAGGTCA

20

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TCGAGGTTCA GAGCGTAGTG

20

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TCTTGGATCT CTGGCACCTC

20

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CCATCAGAGT GAAGGAGGAG

20

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CCATCTTCCA CTGGTCAGAG

20

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CTCCTTCTCT TGGATCTCTG

20

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TTACTTCAGC ACTGTTAGTC

20

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

AGGGAGGGTAG CTCAAAGCTC

20

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TGGGTCCACA GTTCCGACAG

20

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CAACTCTGTG ATGGCTCCAG

20

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

AGCAGGGTTC TGTTCAAGAC

20

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CCATTGGGTG CTAGTCTCTC

20

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

CAGCCATGCT GTCCCAGCAG

20

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CTGGACCTGA GGTAGCGCTG

20

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATAACCACCC TGAGGCAC TG

20

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CCTGCAGGTC GACACTAGTG

20

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

AATTGGAATG AGGAGGACTG

20

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GCTCTAGAAG TACTCTCGAG

20

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ATTGTATGAC AATGCACCAAG

20

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

TCCACAGAGG CCTTCATCAC

20

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

CCTGACTGGC CTAAGCACAG

20

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

AAGCCTCATCA ACCACCACTG

20

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TGTCAACCGT GACAAGTGTG

20

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TTGTACACCA GCTGCAGGTC

20

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GGGTGTGGTG CAGATGAGTC

20

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

ATCACACTCT TATACTCAG

20

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GTGGGAAGCT TTCCTCAGAC

20

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TGATGAACAT GGGCCTGGAG

20

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CATTGTGGAT GTACTACCA

20

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

TGTGTTTGC AACCTGAGTG

20

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

ATAGTGGCAC CACTTACGAG

20

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

AATTCTGCAA CGTGATGGCG

20

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

CACAAAGATGC CTCGTCTGTG

20

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

AATCCGGACA AGGTACAGTC

20

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GCACGAGCTGG CACAAGCCGTG

20

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GCAAGCGTGT GGTGTCACTG

20

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

TGTTTGAAACA GGCTCTGGAC

20

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

CGGCATGGCA ATGAGGACAC

20

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

AGGACGAGAT GGACCTCCAG

20

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CCCTCTGTCC TCTAGGCCAC

20

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

TCTTGAGGGG ACTGACTCTG

20

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

TGAGTGAGGA GGCAGATGTC

20

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

TGGCTTGAA GAAAGAGCTG

20

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GCAAAAGACC AGGCTGACTG

20

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TGCAGCTCCT TGGTCTTCTC

20

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GATTACAGT CCCAAGGCTC

20

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ATCTGGATGA GGCGGTTGAG

20

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GGTCACCTCTC CGACGAGGAG

20

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GGATCCAAAG TTCGTCTCTG

20

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CGCTGTGTGT CTGATCCCTC

20

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ATGAAGGTAA ACCCCCCGGAG

20

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

TGGTCTCTGG CTCTGAGCAC

20

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GCCTGGAGAA GCCCAGTCTG

20

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

CACACTCTGG ACCGTTGCTG

20

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

AAAGCTCCGC AGCCCGAGTG

20

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

TCTTCCAGGA AGCTGCGGTC

20

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

GATGGTGGGG CAGCATTGAG

20

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GTCACCAGTG GTGCCTGCAG

20

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ACCTCACCGT TGCCAACCTG

20

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

CGCAACAGCG TCTCCCTCTG

20

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

AGTACCTTCA TAAGTTCTTC

20

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

TCCCAGACTT CAACCTTCAC

20

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

AAACATCTTC CCGGTCGGAC

20

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GCTGAGCACCC TTTACCTCAC

20

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GACGTCCGTC CGGGAAAGATG

20

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

ACACAGGAGA TGCAGGTCAC

20

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GAGTCTTCCA TGAAGAACAG

20

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GCAGTGAGGA AGGTAAGGAG

20

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4047 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 378...1799
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

GGATCCAAAG GACGCCCCCG CCGACAGGAG AATTGGTCC CGGGCCCGCG GCGATGCC	60
CCCGGTAGCT CGGGCCCGTG GTCGGGTGT TGTGAGTGT TCTATGTGGG AGAAGGAGGA	120
GGAGGAGGAA GAAGAACAA CGATTTGTCT TCTCGGCTGG TCTCCCCCG GCTCTACATG	180
TTCCCGCAC TGAGGAGACG GAAGAGGAGC CGTAGGCCCG CCCCCCTCCCG GCCCCGATTA	240
TAGTCTCTCG CCACAGCGGC CTCGGCCTCC CTTGGATTG AGACGCCGAT TCGCCCAGTG	300
TTGGGAAAT GGGAAAGTAAT GACAGCTGGC ACCTGAACTA AGTACTTTA TAGGAAACAC	360
CATTCCAGAA ATTCAAG ATG AAT GGG GAT ATG CCC CAT GTC CCC ATT ACT	410
Met Asn Gly Asp Met Pro His Val Pro Ile Thr	
1 5 10	
ACT CTT GCG GGG ATT GCT AGT CTC ACA GAC CTC CTG AAC CAG CTG CCT	458
Thr Leu Ala Gly Ile Ala Ser Leu Thr Asp Leu Leu Asn Gln Leu Pro	
15 20 25	
CTT CCA TCT CCT TTA CCT GCT ACA ACT ACA AAG AGC CTT CTC TTT AAT	506
Leu Pro Ser Pro Leu Pro Ala Thr Thr Lys Ser Leu Leu Phe Asn	
30 35 40	
GCA CGA ATA GCA GAA GAG GTG AAC TGC CTT TTG GCT TGT AGG GAT GAC	554
Ala Arg Ile Ala Glu Glu Val Asn Cys Leu Leu Ala Cys Arg Asp Asp	
45 50 55	
AAT TTG GTT TCA CAG CTT GTC CAT AGC CTC AAC CAG GTA TCA ACA GAT	602
Asn Leu Val Ser Gln Leu Val His Ser Leu Asn Gln Val Ser Thr Asp	
60 65 70 75	
CAC ATA GAG TTG AAA GAT AAC CTT GGC AGT GAT GAC CCA GAA GGT GAC	650
His Ile Glu Leu Lys Asp Asn Leu Gly Ser Asp Asp Pro Glu Gly Asp	
80 85 90	
ATA CCA GTC TTG TTG CAG GCC GTC CTG GCA AGG AGT CCT AAT GTT TTC	698
Ile Pro Val Leu Leu Gln Ala Val Leu Ala Arg Ser Pro Asn Val Phe	
95 100 105	
AGG GAG AAA AGC ATG CAG AAC AGA TAT GTC CAA AGT GGA ATG ATG ATG	746
Arg Glu Lys Ser Met Gln Asn Arg Tyr Val Gln Ser Gly Met Met Met	
110 115 120	
TCT CAG TAT AAA CTT TCT CAG AAT TCC ATG CAC AGT AGT CCT GCA TCT	794
Ser Gln Tyr Lys Leu Ser Gln Asn Ser Met His Ser Ser Pro Ala Ser	
125 130 135	
TCC AAT TAT CAA CAA ACC ACT ATC TCA CAT AGC CCC TCC AGC CGG TTT	842
Ser Asn Tyr Gln Gln Thr Thr Ile Ser His Ser Pro Ser Ser Arg Phe	
140 145 150 155	
GTG CCA CCA CAG ACA AGC TCT GGG AAC AGA TTT ATG CCA CAG CAA AAT	890
Val Pro Pro Gln Thr Ser Ser Gly Asn Arg Phe Met Pro Gln Gln Asn	
160 165 170	
AGC CCA GTG CCT AGT CCA TAC GCC CCA CAA AGC CCT GCA GGA TAC ATG	938
Ser Pro Val Pro Ser Pro Tyr Ala Pro Gln Ser Pro Ala Gly Tyr Met	
175 180 185	
CCA TAT TCC CAT CCT TCA AGT TAC ACA ACA CAT CCA CAG ATG CAA CAA	986
Pro Tyr Ser His Pro Ser Ser Tyr Thr Thr His Pro Gln Met Gln Gln	
190 195 200	

GCA TCG GTA TCA AGT CCC ATT GTT GCA GGT GGT TTG AGA AAC ATA CAT Ala Ser Val Ser Ser Pro Ile Val Ala Gly Gly Leu Arg Asn Ile His 205 210 215	1034
GAT AAT AAA GTT TCT GGT CCG TTG TCT GGC AAT TCA GCT AAT CAT CAT Asp Asn Lys Val Ser Gly Pro Leu Ser Gly Asn Ser Ala Asn His His 220 225 230 235	1082
GCT GAT AAT CCT AGA CAT GGT TCA AGT GAG GAC TAC CTA CAC ATG GTG Ala Asp Asn Pro Arg His Gly Ser Ser Glu Asp Tyr Leu His Met Val 240 245 250	1130
CAC AGG CTA AGT AGT GAC GAT GGA GAT TCT TCA ACA ATG AGG AAT GCT His Arg Leu Ser Ser Asp Asp Gly Asp Ser Ser Thr Met Arg Asn Ala 255 260 265	1178
GCA TCT TTT CCC TTG AGA TCT CCA CAG CCA GTA TGC TCC CCT GCT GGA Ala Ser Phe Pro Leu Arg Ser Pro Gln Pro Val Cys Ser Pro Ala Gly 270 275 280	1226
AGT GAA GGA ACT CCT AAA GGC TCA AGA CCA CCT TTA ATC CTA CAA TCT Ser Glu Gly Thr Pro Lys Gly Ser Arg Pro Pro Leu Ile Leu Gln Ser 285 290 295	1274
CAG TCT CTA CCT TGT TCA TCA CCT CGA GAT GTT CCA CCA GAT ATC TTG Gln Ser Leu Pro Cys Ser Ser Pro Arg Asp Val Pro Pro Asp Ile Leu 300 305 310 315	1322
CTA GAT TCT CCA GAA AGA AAA CAA AAG AAG CAG AAG AAA ATG AAA TTA Leu Asp Ser Pro Glu Arg Lys Gln Lys Lys Gln Lys Lys Met Lys Leu 320 325 330	1370
GGC AAG GAT GAA AAA GAG CAG AGT GAG AAA GCG GCA ATG TAT GAT ATA Gly Lys Asp Glu Lys Glu Gln Ser Glu Lys Ala Ala Met Tyr Asp Ile 335 340 345	1418
ATT AGT TCT CCA TCC AAG GAC TCT ACT AAA CTT ACA TTA AGA CTT TCT Ile Ser Ser Pro Ser Lys Asp Ser Thr Lys Leu Thr Leu Arg Leu Ser 350 355 360	1466
CGT GTA AGG TCT TCA GAC ATG GAC CAG CAA GAG GAT ATG ATT TCT GGT Arg Val Arg Ser Ser Asp Met Asp Gln Gln Glu Asp Met Ile Ser Gly 365 370 375	1514
GTG GAA AAT AGC AAT GTT TCA GAA AAT GAT ATT CCT TTT AAT GTG CAG Val Glu Asn Ser Asn Val Ser Glu Asn Asp Ile Pro Phe Asn Val Gln 380 385 390 395	1562
TAC CCA GGA CAG ACT TCA AAA ACA CCC ATT ACT CCA CAA GAT ATA AAC Tyr Pro Gly Gln Thr Ser Lys Thr Pro Ile Thr Pro Gln Asp Ile Asn 400 405 410	1610
CGC CCA CTA AAT GCT GCT CAA TGT TTG TCG CAG CAA GAA CAA ACA GCA Arg Pro Leu Asn Ala Ala Gln Cys Leu Ser Gln Gln Glu Gln Thr Ala 415 420 425	1658
TTC CTT CCA GCA AAT CAA GTG CCT GTT TTA CAA CAG AAC ACT TCA GTT Phe Leu Pro Ala Asn Gln Val Pro Val Leu Gln Gln Asn Thr Ser Val 430 435 440	1706
GCT GCA AAA CAA CCC CAG ACC AAT AGT CAC AAA ACC TTG GTG CAG CCT Ala Ala Lys Gln Pro Gln Thr Asn Ser His Lys Thr Leu Val Gln Pro 445 450 455	1754
GGA ACA GGC ATA GAG GTC TCA GCA GAG CTG CCC AAG GAC AAG ACC TAAGA Gly Thr Gly Ile Glu Val Ser Ala Glu Leu Pro Lys Asp Lys Thr 460 465 470	1804
TCCAGCAGGG AACTATGTAG TCACCCCGAG AGGCCAGCT CTCTCCGTGA GCTCTGGGCC TAGGGTGGGG GTGGTTGTTG GTTCTGCGCG CACTGTTCCC CCTACATGAT GGGTCCATCC CAGTTGGCTT CTCTCACTCC CTTCCTCTG TGGAGAAGCC TTGCCAGGTG TCACTGCTC CAGGAAGCTG TCTCTGATTG CTCCAGTTGA ACAGTGAGAT TTGCCACACC TCACATGCAT CGCTCTGTC CCTGGATTG TAACCATAGG TTTTCTGTC TCCTGGAGGA CAAGGATGAG	1864 1924 1984 2044 2104

GGCTTCCAC	TTGAGTCTCC	CTGGTGGAGC	CCAGCTCTG	ACATACCTG	TAAGAGTCT	2164
CAAGAGAAGA	ACATGGAGGA	GGAAATGTGGA	TAACAACCC	GGCTGCCTG	GTGTTCCAAG	2224
CTAGGAAGAT	GTAAATGTCCC	CACAAACGGG	GTAATGGCT	TGCCTGCCTC	ACAGCTGTCT	2284
CAAGGCCAGG	CCCTGGCCG	CAGCCAAGC	CCAAGGACTA	GTCAGGAGC	CACACAGGCC	2344
CAGGCCACAT	CCGCCTCAC	TGGGACCTT	TGTGGGGTAC	AGTCTCCGGC	CCCACCCAGA	2404
CCTCCTGAAG	GAGAGACCC	ATGCAAGGA	CTCACCCACC	TGCACTTCA	TAAGCCCCA	2464
GTGGGTTCT	AGGCATGAAG	ACCAACGGTT	AGAGGCTGAA	CTGGCAGGAA	CCTGTCTCCA	2524
GCCCCCTCTC	ACCCCAGCCG	GGCCCTGCCT	CAGAGGCAGC	ACCCAGGACG	TGGCCATGAC	2584
CCGTGGACTC	CACTCAATCC	CTCTCTCCA	GGAGGCATGC	AAAGTGTCA	CCAGCCAGGC	2644
CCCTGGAAAG	CACTCATCAC	CTCTTAAGGC	ATTGTGGGTG	TCGGCTCTGC	AACTGCCAGG	2704
TGCAGCACAC	GACCGGTGTC	CGGTGTTCGA	TAGCAGGGAG	CCATGACCTG	GCAACGATTC	2764
CACGCTCAA	GGGGCACCCC	GGGGCCCTG	GTCAGGGCG	GATCAGCTT	CCCTGGGCAC	2824
ATCTGCTCA	TTCCAGATCT	CCAGGGCTCA	TGTCTGTGAC	AGGGAGGGAA	GGCTCTGCC	2884
TGGCCTTCG	TCAGCTCTGC	CACTGCAGGC	TGGGAGCCT	GGGCTTATA	GCTGGCTTCT	2944
GCCCCACACT	TCTCGTGAAG	AGGAAACCAA	CTATGAGCT	GCCAAACGCA	TCTCAGATGC	3004
GTTTTAAAAA	ATTCTGGTCC	CCCGCTCTG	TCCCATCATC	CCCTCGGGG	ACTTCTCTC	3064
TCCGTGGTTC	TCACCCATA	CTCTGTACT	GCCACATTT	CACCTGGGC	TGGCCTTTGT	3124
CTCCACCTGA	AACTCTGAA	AATCTTGA	TGGATTCTA	GGTCACTGGG	GACTCCGGCA	3184
GCACATTCG	CTTCAGAATA	AAGGGCCCC	GGGGTCCCC	AGCACCTCCC	AAAGCCACAC	3244
CCCTAGCTC	CCTCCCTAC	CCTCGAGCCT	GAGGGTCCC	TCAGCCACCC	TTAAGTCCCC	3304
ACCTGGCTC	CTGCCCCG	CTTGGCTAGC	ACGGGCTCT	CCACCGGGG	CCCTCTGCT	3364
CACAGAGCCC	CCTCACCTCC	CTGGGGATGA	GGGGCCAGGC	CATGACCTG	AAAGTCTAGC	3424
CCTGGCCTC	ACCTCCCAGG	AGGCCCTCC	CCGCCCTCTC	CCGGCCCCGG	CCCGTCCCTC	3484
TGCTGCTGGC	CTCTGGTGC	TGCCCGCAG	ACTGAGETGC	GCTTGGGGT	CCTGGCGGCC	3544
TGGGGCGTCC	CGCAGCGAAC	CCAGGCGGTG	GGAGCCCGGC	GGGAAGGC	GAGGTCCTTC	3604
TGGGGGCTCC	TCCGACGCT	GAGGGCGCTG	CTTCCCCCGG	GCCCCCCCCG	GTTTCTGCGG	3664
AGCCCCGGCC	TCCGCTCTG	GGTGACCCGG	TGAGACCCCC	GGGGAGGGCG	CTGGGGAGGC	3724
CGGGGCTCTG	CTCCCGGGTC	CCAAACGAC	TGGCTGCC	TCAGGAGGGA	CGGGCACCTC	3784
CACCCACGGC	GCTGGCCGCC	GCACGGCCGC	TCCCTCCGCT	CCCGCAGCCT	GGACGCCCTC	3844
CGAGGGCGCC	CCGGCGGCC	CCACGCGCG	CCCCATCCGC	AGGCCAGGAC	TGCCCTCCCG	3904
GAGCTGGCGG	CCCCCAGCCT	GGAGGAGCGG	GGCCCGAGACG	CCCTCCCAGC	CTCCCCAGC	3964
CCACTCTGGC	CCCCCAGCCC	CCCCCTGGTC	CGAGTGC	TCTCTGGCCC	CGGCCTTCC	4024
CGGGGAAGGA	AAGCAAAAG	CTT				4047

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Met	Asn	Gly	Asp	Met	Pro	His	Val	Pro	Ile	Thr	Thr	Leu	Ala	Gly	Ile
1				5				10				15			
Ala	Ser	Leu	Thr	Asp	Leu	Leu	Asn	Gln	Leu	Pro	Leu	Pro	Ser	Pro	Leu
					20			25			30				
Pro	Ala	Thr	Thr	Thr	Lys	Ser	Leu	Leu	Phe	Asn	Ala	Arg	Ile	Ala	Glu
					35			40			45				
Glu	Val	Asn	Cys	Leu	Leu	Ala	Cys	Arg	Asp	Asp	Asn	Leu	Val	Ser	Gln
					50			55			60				
Leu	Val	His	Ser	Leu	Asn	Gln	Val	Ser	Thr	Asp	His	Ile	Glu	Leu	Lys
					65			70			75			80	
Asp	Asn	Leu	Gly	Ser	Asp	Asp	Pro	Glu	Gly	Asp	Ile	Pro	Val	Leu	
					85			90			95				
Gln	Ala	Val	Leu	Ala	Arg	Ser	Pro	Asn	Val	Phe	Arg	Glu	Lys	Ser	Met
					100			105			110				
Gln	Asn	Arg	Tyr	Val	Gln	Ser	Gly	Met	Met	Met	Ser	Gln	Tyr	Lys	Leu
					115			120			125				
Ser	Gln	Asn	Ser	Met	His	Ser	Ser	Pro	Ala	Ser	Ser	Asn	Tyr	Gln	Gln
					130			135			140				
Thr	Thr	Ile	Ser	His	Ser	Pro	Ser	Ser	Arg	Phe	Val	Pro	Pro	Gln	Thr
					145			150			155			160	
Ser	Ser	Gly	Asn	Arg	Phe	Met	Pro	Gln	Gln	Asn	Ser	Pro	Val	Pro	Ser
					165			170			175				
Pro	Tyr	Ala	Pro	Gln	Ser	Pro	Ala	Gly	Tyr	Met	Pro	Tyr	Ser	His	Pro
					180			185			190				
Ser	Ser	Tyr	Thr	Thr	His	Pro	Gln	Met	Gln	Gln	Ala	Ser	Val	Ser	Ser
					195			200			205				

Pro Ile Val Ala Gly Gly Leu Arg Asn Ile His Asp Asn Lys Val Ser
 210 215 220
 Gly Pro Leu Ser Gly Asn Ser Ala Asn His His Ala Asp Asn Pro Arg
 225 230 235 240
 His Gly Ser Ser Glu Asp Tyr Leu His Met Val His Arg Leu Ser Ser
 245 250 255
 Asp Asp Gly Asp Ser Ser Thr Met Arg Asn Ala Ala Ser Phe Pro Leu
 260 265 270
 Arg Ser Pro Gln Pro Val Cys Ser Pro Ala Gly Ser Glu Gly Thr Pro
 275 280 285
 Lys Gly Ser Arg Pro Pro Leu Ile Leu Gln Ser Gln Ser Leu Pro Cys
 290 295 300
 Ser Ser Pro Arg Asp Val Pro Pro Asp Ile Leu Leu Asp Ser Pro Glu
 305 310 315 320
 Arg Lys Gln Lys Gln Lys Lys Met Lys Leu Gly Lys Asp Glu Lys
 325 330 335
 Glu Gln Ser Glu Lys Ala Ala Met Tyr Asp Ile Ile Ser Ser Pro Ser
 340 345 350
 Lys Asp Ser Thr Lys Leu Thr Leu Arg Leu Ser Arg Val Arg Ser Ser
 355 360 365
 Asp Met Asp Gln Gln Glu Asp Met Ile Ser Gly Val Glu Asn Ser Asn
 370 375 380
 Val Ser Glu Asn Asp Ile Pro Phe Asn Val Gln Tyr Pro Gly Gln Thr
 385 390 395 400
 Ser Lys Thr Pro Ile Thr Pro Gln Asp Ile Asn Arg Pro Leu Asn Ala
 405 410 415
 Ala Gln Cys Leu Ser Gln Gln Glu Gln Thr Ala Phe Leu Pro Ala Asn
 420 425 430
 Gln Val Pro Val Leu Gln Gln Asn Thr Ser Val Ala Ala Lys Gln Pro
 435 440 445
 Gln Thr Asn Ser His Lys Thr Leu Val Gln Pro Gly Thr Gly Ile Glu
 450 455 460
 Val Ser Ala Glu Leu Pro Lys Asp Lys Thr
 465 470

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 26...799
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

AAGCTTTTG AATTGGCAC GAGAT GCT ACA CAG GCT ATA TTT GAA ATA CTG	52
Ala Thr Gln Ala Ile Phe Glu Ile Leu	
1 5	
GAG AAA TCC TGG TTG CCC CAG AAT TGT ACA CTG GTT GAT ATG AAG ATT	100
Glu Lys Ser Trp Leu Pro Gln Asn Cys Thr Leu Val Asp Met Lys Ile	
10 15 20 25	
GAA TTT GGT GTT GAT GTA ACC ACC AAA GAA ATT GTT CTT GCT GAT GTT	148
Glu Phe Gly Val Asp Val Thr Thr Lys Glu Ile Val Leu Ala Asp Val	
30 35 40	
ATT GAC AAT GAT TCC TGG AGA CTC TGG CCA TCA GGA GAT CGA AGC CAA	196
Ile Asp Asn Asp Ser Trp Arg Leu Trp Pro Ser Gly Asp Arg Ser Gln	
45 50 55	
CAG AAA GAC AAA CAG TCT TAT CGG GAC CTC AAA GAA GTA ACT CCT GAA	244
Gln Lys Asp Lys Gln Ser Tyr Arg Asp Leu Lys Glu Val Thr Pro Glu	
60 65 70	
GGG CTC CAA ATG GTA AAG AAA AAC TTT GAG TGG GTT GCA GAG AGA GTA	292

Gly Leu Gln Met Val Lys Lys Asn Phe Glu Trp Val Ala Glu Arg Val			
75	80	85	
GAG TTG CTT TTG AAA TCA GAA AGT CAG TGC AGG GTT GTA GTG TTG ATG			340
Glu Leu Leu Leu Lys Ser Glu Ser Gln Cys Arg Val Val Val Leu Met			
90	95	100	105
GGC TCT ACT TCT GAT CTT GGT CAC TGT GAA AAA ATC AAG AAG GCC TGT			388
Gly Ser Thr Ser Asp Leu Gly His Cys Glu Lys Ile Lys Lys Ala Cys			
110	115	120	
GGA AAT TTT GGC ATT CCA TGT GAA CTT CGA GTA ACA TCT GCG CAT AAA			436
Gly Asn Phe Gly Ile Pro Cys Glu Leu Arg Val Thr Ser Ala His Lys			
125	130	135	
GGA CCA GAT GAA ACT CTG AGG ATT AAA GCT GAG TAT GAA GGG GAT GGC			484
Gly Pro Asp Glu Thr Leu Arg Ile Lys Ala Glu Tyr Glu Gly Asp Gly			
140	145	150	
ATT CCT ACT GTA TTT GTG GCA GTG GCA GGC AGA AGT AAT GGT TTG GGA			532
Ile Pro Thr Val Phe Val Ala Val Ala Gly Arg Ser Asn Gly Leu Gly			
155	160	165	
CCA GTG ATG TCT GGG AAC ACT GCA TAT CCA GTT ATC AGC TGT CCT CCC			580
Pro Val Met Ser Gly Asn Thr Ala Tyr Pro Val Ile Ser Cys Pro Pro			
170	175	180	185
CTC ACA CCA GAC TGG GGA GTT CAG GAT GTG TGG TCT TCT CTT CGA CTA			628
Leu Thr Pro Asp Trp Gly Val Gln Asp Val Trp Ser Ser Leu Arg Leu			
190	195	200	
CCC AGT GGT CTT GGC TGT TCA ACC GTA CTT TCT CCA GAA GGA TCA GCT			676
Pro Ser Gly Leu Gly Cys Ser Thr Val Leu Ser Pro Glu Gly Ser Ala			
205	210	215	
CAA TTT GCT GCT CAG ATA TTT GGG TTA AGC AAC CAT TTG GTA TGG AGC			724
Gln Phe Ala Ala Gln Ile Phe Gly Leu Ser Asn His Leu Val Trp Ser			
220	225	230	
AAA CTG CGA GCA AGC ATT TTG AAC ACA TGG ATT TCC TTG AAG CAG GCT			772
Lys Leu Arg Ala Ser Ile Leu Asn Thr Trp Ile Ser Leu Lys Gln Ala			
235	240	245	
GAC AAG AAA ATC AGA GAA TGT AAT TTA TAAGAAAGAA TGCCATTGAA TTTTTTA			826
Asp Lys Lys Ile Arg Glu Cys Asn Leu			
250	255		
GGGGAAAAAC TACAAATTTC TAATTTAGCT GAAGGAAAAT CAAGCAAGAT GAAAAGGTA			886
TTTTAAATTA GAGAACACAA ATAAAATGTA TTACTGAATA ATGGTGAGG GTAGGCCTAT			946
TCAGATGCAA GGGCAGCAAT GGGGCTCCCC ATTATCCCCA CCCCCTTGGT CCCAGTCCCC			1006
TTCTCTGCAA TGGGCACGCA TAGAGGAGAG ACAAAAGGTA TTAGACGCAA CATCATGGC			1066
CCAGGGGAGT CCGAGAAGAG CTGGCATTGG CTGACAGGGC ATTTTCAGGC TCTGTCTTG			1126
GTCAGGGAGC ACACCCCGAC CTGAAGAGTG ATGCCATTGG CCAGGGAGTG GTTTGTCTAT			1186
AGCCGTTGCC TGTGAAGTGG AAGGAAAAAGA TCTGGAAATG AAGCCCTGTG GCCAGGAAGA			1246
TAGACAGGGC AGCAACTTCT GGGCCTCCAG GCCCCCTTCCC CACCATAGCA ATGTGGCAGA			1306
AACTGGTGTG AGGCCCCAGC CAGAAAAAAGG AGCCCAAGGCC AGAGGGCAAG TGACAAAGGA			1366
TGTACCATGT CCAATCTCCC ACACCCCTGGG GCTGCCCTTC CCAATGTCTT TCTTGATAGC			1426
CAAGTTGGGC TGGGAGCAGC TCACCTGCTC TCTAGCCAGG AGGGTTCTC AGCTCCCTGGA			1486
GGCCGCTAGCT TGATGTTGAA CTGCTGCAGG GTCTGCTCCA GCTGTTCTG GTTCCCAGCA			1546
AAGTAGGGGG ACACAGCATT GTGGAAGAGC AGCACGCTGT TGTCATCAC CTTGATCTTG			1606
TTTTCTTCCA GGAACCTTGAG CTTGATGGCC ACATCTCCCC GCAGCTTCTC ATACTGTCC			1666
CGATGGGCCT GGAAGGTGGC CTGGGCACTC TCAAGTCGAC CACGTGTCCC TGCACTCCCG			1726
GGGCCTAGAC TCAGCTCTC TAAGTCTGTT CGGTAGGCAT CATATTCCAG CCTGGCAGCC			1786
TCATACTGT TCACAGTCAT GAGCCGTGTCT TCCATGGCTC TGGTGACCAA TGTGTTGATG			1846
CTAGAGACAA AGAAGTTCAC GGCTCTAGC AGCCTTCCC CATTCTTGC TAGTAGTTTC			1906
TGTGTCTCTG CATTGTTAGCC AAATTCCTCC TGAAGCTCTG GGGACTTCTG GCTGAGGTCA			1966
GCAAAGGCAT CACCCAGTGC ATGCTGGGTG TGCAAGCAGGC TGAGGGGT GGCTGTCAGT			2026
GCCCCGGCCA GCTGCAGGAC ACTCTCATAC TTGCGCTTCC TCTCACGCAG CAACTCAATC			2086
TGCACTCTA GCTCCAGGAT TCCGGCGCCT CCACCTCCGTC CCCCCGGGGT CTGCTCTGTG			2146
TGCCATGGAC GGCATTGTC CAGATATAGC CGTTGTCAGA AAGCGGGGAT CTGACCGAGCT			2206
TTTCTCTACT TGTGTCACTA ACGGACCGTT TATCATGAGC AGCAACTCGG CTTCTGCAGC			2266
AAACGGAAAT GACAGCAAGA AGTCAAAGG TGACAGCCGA AGTGCAGGGCG TCCCCCTCTAG			2326
AGTGATCCAC ATCCGGAAGC TCCCCATCGA CGTCACGGAG GGGGAAGTCA TCTCCCTGGG			2386

GCTGCCCTT	GGGAAGGTCA	CCAACCTCCT	GATGCTGAAG	GGGAAAACC	AGGCCTTCAT	2446
CGAGATGAAC	ACCGAGGAGG	CTGCCAATAC	CATGGTGAAC	TACTACACCT	CGGTGACCCC	2506
TGTGCTGCC	GGCCAGCCA	TCTACATCCA	GTTCCTCCAAC	CACAAGGAGC	TGAAGACCGA	2566
CAGCTCTCC	AACCAAGGCC	GGGGCCAGGC	GGCCCTGCAG	CGGGTGAACT	CGGTCCAGTC	2626
GGGGAACCTG	GCCTTGGCTG	CCTCGCGGC	GGCCGTGGAT	GCAGGGATGG	CGATGCCGG	2686
GCAGAGCCCC	GTGCTCAGGA	TCATCGTGG	GAACCTCTTC	TACCCGTGTA	CCCTGGATGT	2746
GCTGCACCAG	ATTTCTCCA	AGTTCGGCAC	AGTGTGAAG	ATCATCACCT	TCACCAAGAA	2806
CAACCAGTC	CAGGCCCTGC	TGCAGTATGC	GGACCCCGTG	AGCGCCCAGC	ACGCCAAGCT	2866
GTCCGTTGGAC	GGGCAGAAC	TCTACAACGC	CTGCTGCAGC	CTGCCATCG	ACTTTCCAA	2926
GCTCACCAAGC	CTCAACGTCA	AGTACAACAA	TGACAAGAGC	C GTGACTACC	TCGTGCCGAA	2986
TTCTTGGAT	CC					2998

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Ala	Thr	Gln	Ala	Ile	Phe	Glu	Ile	Leu	Glu	Ser	Trp	Leu	Pro	Gln	
1				5			10					15			
Asn	Cys	Thr	Leu	Val	Asp	Met	Lys	Ile	Glu	Phe	Gly	Val	Asp	Val	Thr
						20		25				30			
Thr	Lys	Glu	Ile	Val	Leu	Ala	Asp	Val	Ile	Asp	Asn	Asp	Ser	Trp	Arg
						35		40			45				
Leu	Trp	Pro	Ser	Gly	Asp	Arg	Ser	Gln	Gln	Lys	Asp	Lys	Gln	Ser	Tyr
						50		55			60				
Arg	Asp	Leu	Lys	Glu	Val	Thr	Pro	Glu	Gly	Leu	Gln	Met	Val	Lys	Lys
						65		70		75		80			
Asn	Phe	Glu	Trp	Val	Ala	Glu	Arg	Val	Glu	Leu	Leu	Leu	Lys	Ser	Glu
						85		90			95				
Ser	Gln	Cys	Arg	Val	Val	Val	Leu	Met	Gly	Ser	Thr	Ser	Asp	Leu	Gly
						100		105			110				
His	Cys	Glu	Ile	Lys	Lys	Ala	Cys	Gly	Asn	Phe	Gly	Ile	Pro	Cys	
						115		120			125				
Glu	Leu	Arg	Val	Thr	Ser	Ala	His	Lys	Gly	Pro	Asp	Glu	Thr	Leu	Arg
						130		135			140				
Ile	Lys	Ala	Glu	Tyr	Glu	Gly	Asp	Gly	Ile	Pro	Thr	Val	Phe	Val	Ala
						145		150			155			160	
Val	Ala	Gly	Arg	Ser	Asn	Gly	Leu	Gly	Pro	Val	Met	Ser	Gly	Asn	Thr
						165		170			175				
Ala	Tyr	Pro	Val	Ile	Ser	Cys	Pro	Pro	Leu	Thr	Pro	Asp	Trp	Gly	Val
						180		185			190				
Gln	Asp	Val	Trp	Ser	Ser	Leu	Arg	Leu	Pro	Ser	Gly	Leu	Gly	Cys	Ser
						195		200			205				
Thr	Val	Leu	Ser	Pro	Glu	Gly	Ser	Ala	Gln	Phe	Ala	Ala	Gln	Ile	Phe
						210		215			220				
Gly	Leu	Ser	Asn	His	Leu	Val	Trp	Ser	Lys	Leu	Arg	Ala	Ser	Ile	Leu
						225		230			235			240	
Asn	Thr	Trp	Ile	Ser	Leu	Lys	Gln	Ala	Asp	Lys	Lys	Ile	Arg	Glu	Cys
						245		250			255				
Asn	Leu														

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1038 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Ile	Gln	Arg	Phe	Gly	Thr	Ser	Gly	His	Ile	Met	Asn	Leu	Gln	Ala	Gln
1					5				10				15		

Pro Lys Ala Gln Asn Lys Arg Lys Arg Cys Leu Phe Gly Gly Gln Glu
 20 25 30
 Pro Ala Pro Lys Glu Gln Pro Pro Pro Leu Gln Pro Pro Gln Gln Ser
 35 40 45
 Ile Arg Val Lys Glu Glu Gln Tyr Leu Gly His Glu Gly Pro Gly Gly
 50 55 60
 Ala Val Ser Thr Ser Gln Pro Val Glu Leu Pro Pro Pro Ser Ser Leu
 65 70 75 80
 Ala Leu Leu Asn Ser Val Val Tyr Gly Pro Glu Arg Thr Ser Ala Ala
 85 90 95
 Met Leu Ser Gln Gln Val Ala Ser Val Lys Trp Pro Asn Ser Val Met
 100 105 110
 Ala Pro Gly Arg Gly Pro Glu Arg Gly Gly Gly Val Ser Asp
 115 120 125
 Ser Ser Trp Gln Gln Pro Gly Gln Pro Pro Pro His Ser Thr Trp
 130 135 140
 Asn Cys His Ser Leu Ser Leu Tyr Ser Ala Thr Lys Gly Ser Pro His
 145 150 155 160
 Pro Gly Val Gly Val Pro Thr Tyr Tyr Asn His Pro Glu Ala Leu Lys
 165 170 175
 Arg Glu Lys Ala Gly Gly Pro Gln Leu Asp Arg Tyr Val Arg Pro Met
 180 185 190
 Met Pro Gln Lys Val Gln Leu Glu Val Gly Arg Pro Gln Ala Pro Leu
 195 200 205
 Asn Ser Phe His Ala Ala Lys Lys Pro Pro Asn Gln Ser Leu Pro Leu
 210 215 220
 Gln Pro Phe Gln Leu Ala Phe Gly His Gln Val Asn Arg Gln Val Phe
 225 230 235 240
 Arg Gln Gly Pro Pro Pro Asn Pro Val Ala Ala Phe Pro Pro Gln
 245 250 255
 Lys Gln Gln Gln Gln Gln Pro Gln Gln Gln Gln Gln Gln Gln
 260 265 270
 Ala Ala Leu Pro Gln Met Pro Leu Phe Glu Asn Phe Tyr Ser Met Pro
 275 280 285
 Gln Gln Pro Ser Gln Gln Pro Gln Asp Phe Gly Leu Gln Pro Ala Gly
 290 295 300
 Pro Leu Gly Gln Ser His Leu Ala His His Ser Met Ala Pro Tyr Pro
 305 310 315 320
 Phe Pro Pro Asn Pro Asp Met Asn Pro Glu Leu Arg Lys Ala Leu Leu
 325 330 335
 Gln Asp Ser Ala Pro Gln Pro Ala Leu Pro Gln Val Gln Ile Pro Phe
 340 345 350
 Pro Arg Arg Ser Arg Arg Leu Ser Lys Glu Gly Ile Leu Pro Pro Ser
 355 360 365
 Ala Leu Asp Gly Ala Gly Thr Gln Pro Gly Gln Glu Ala Thr Gly Asn
 370 375 380
 Leu Phe Leu His His Trp Pro Leu Gln Gln Pro Pro Pro Gly Ser Leu
 385 390 395 400
 Gly Gln Pro His Pro Glu Ala Leu Gly Phe Pro Leu Glu Leu Arg Glu
 405 410 415
 Ser Gln Leu Leu Pro Asp Gly Glu Arg Leu Ala Pro Asn Gly Arg Glu
 420 425 430
 Arg Glu Ala Pro Ala Met Gly Ser Glu Glu Gly Met Arg Ala Val Ser
 435 440 445
 Thr Gly Asp Cys Gly Gln Val Leu Arg Gly Gly Val Ile Gln Ser Thr
 450 455 460
 Arg Arg Arg Arg Ala Ser Gln Glu Ala Asn Leu Leu Thr Leu Ala
 465 470 475 480
 Gln Lys Ala Val Glu Leu Ala Ser Leu Gln Asn Ala Lys Asp Gly Ser
 485 490 495
 Gly Ser Glu Glu Lys Arg Lys Ser Val Leu Ala Ser Thr Thr Lys Cys
 500 505 510
 Gly Val Glu Phe Ser Glu Pro Ser Leu Ala Thr Lys Arg Ala Arg Glu
 515 520 525
 Asp Ser Gly Met Val Pro Leu Ile Ile Pro Val Ser Val Pro Val Arg
 530 535 540
 Thr Val Asp Pro Thr Glu Ala Ala Gln Ala Gly Gly Leu Asp Glu Asp
 545 550 555 560
 Gly Lys Gly Leu Glu Gln Asn Pro Ala Glu His Lys Pro Ser Val Ile
 565 570 575
 Val Thr Arg Arg Arg Ser Thr Arg Ile Pro Gly Thr Asp Ala Gln Ala
 580 585 590
 Gln Ala Glu Asp Met Asn Val Lys Leu Glu Gly Glu Pro Ser Val Arg

595	600	605
Lys Pro Lys Gln Arg Pro Arg Pro Glu Pro Leu Ile Ile Pro Thr Lys		
610	615	620
Ala Gly Thr Phe Ile Ala Pro Pro Val Tyr Ser Asn Ile Thr Pro Tyr		
625	630	635
Gln Ser His Leu Arg Ser Pro Val Arg Leu Ala Asp His Pro Ser Glu		
645	650	655
Arg Ser Phe Glu Leu Pro Pro Tyr Thr Pro Pro Pro Ile Leu Ser Pro		
660	665	670
Val Arg Glu Gly Ser Gly Leu Tyr Phe Asn Ala Ile Ile Ser Thr Ser		
675	680	685
Thr Ile Pro Ala Pro Pro Ile Thr Pro Lys Ser Ala His Arg Thr		
690	695	700
Leu Leu Arg Thr Asn Ser Ala Glu Val Thr Pro Pro Val Leu Ser Val		
705	710	715
Met Gly Glu Ala Thr Pro Val Ser Ile Glu Pro Arg Ile Asn Val Gly		
725	730	735
Ser Arg Phe Gln Ala Glu Ile Pro Leu Met Arg Asp Arg Ala Leu Ala		
740	745	750
Ala Ala Asp Pro His Lys Ala Asp Leu Val Trp Gln Pro Trp Glu Asp		
755	760	765
Leu Glu Ser Ser Arg Glu Lys Gln Arg Gln Val Glu Asp Leu Leu Thr		
770	775	780
Ala Ala Cys Ser Ser Ile Phe Pro Gly Ala Gly Thr Asn Gln Glu Leu		
785	790	795
Ala Leu His Cys Leu His Glu Ser Arg Gly Asp Ile Leu Glu Thr Leu		
805	810	815
Asn Lys Leu Leu Lys Lys Pro Leu Arg Pro His Asn His Pro Leu		
820	825	830
Ala Thr Tyr His Tyr Thr Gly Ser Asp Gln Trp Lys Met Ala Glu Arg		
835	840	845
Lys Leu Phe Asn Lys Gly Ile Ala Ile Tyr Lys Lys Asp Phe Phe Leu		
850	855	860
Val Gln Lys Leu Ile Gln Thr Lys Thr Val Ala Gln Cys Val Glu Phe		
865	870	875
Tyr Tyr Thr Tyr Lys Lys Gln Val Lys Ile Gly Arg Asn Gly Thr Leu		
885	890	895
Thr Phe Gly Asp Val Asp Thr Ser Asp Glu Lys Ser Ala Gln Glu Glu		
900	905	910
Val Glu Val Asp Ile Lys Thr Ser Gln Lys Phe Pro Arg Val Pro Leu		
915	920	925
Pro Arg Arg Glu Ser Pro Ser Glu Glu Arg Leu Glu Pro Lys Arg Glu		
930	935	940
Val Lys Glu Pro Arg Lys Glu Gly Glu Glu Glu Val Pro Glu Ile Gln		
945	950	955
Glu Lys Glu Glu Gln Glu Glu Gly Arg Glu Arg Ser Arg Arg Ala Ala		
965	970	975
Ala Val Lys Ala Thr Gln Thr Leu Gln Ala Asn Glu Ser Ala Ser Asp		
980	985	990
Ile Leu Ile Leu Arg Ser His Glu Ser Asn Ala Pro Gly Ser Ala Gly		
995	1000	1005
Gly Gln Ala Ser Glu Lys Pro Arg Glu Gly Thr Gly Lys Ser Arg Arg		
1010	1015	1020
Ala Leu Pro Phe Ser Glu Lys Lys Lys Lys Gln Lys Ala		
1025	1030	1035

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Ile Arg His Glu Val Ser Phe Leu Trp Asn Thr Glu Ala Ala Cys Pro		
1	5	10
Ile Gln Thr Thr Thr Asp Thr Asp Gln Ala Cys Ser Ile Arg Asp Pro		
20	25	30
Asn Ser Gly Phe Val Phe Asn Leu Asn Pro Leu Asn Ser Ser Gln Gly		
35	40	45

Tyr Asn Val Ser Gly Ile Gly Lys Ile Phe Met Phe Asn Val Cys Gly
 50 55 60
 Thr Met Pro Val Cys Gly Thr Ile Leu Gly Lys Pro Ala Ser Gly Cys
 65 70 75 80
 Glu Ala Glu Thr Gln Thr Glu Glu Leu Lys Asn Trp Lys Pro Ala Arg
 85 90 95
 Pro Val Gly Ile Glu Lys Ser Leu Gln Leu Ser Thr Glu Gly Phe Ile
 100 105 110
 Thr Leu Thr Tyr Lys Gly Pro Leu Ser Ala Lys Gly Thr Ala Asp Ala
 115 120 125
 Phe Ile Val Arg Phe Val Cys Asn Asp Asp Val Tyr Ser Gly Pro Leu
 130 135 140
 Lys Phe Leu His Gln Asp Ile Asp Ser Gly Gln Gly Ile Arg Asn Thr
 145 150 155 160
 Tyr Phe Glu Phe Glu Thr Ala Leu Ala Cys Val Pro Ser Pro Val Asp
 165 170 175
 Cys Gln Val Thr Asp Leu Ala Gly Asn Glu Tyr Asp Leu Thr Gly Leu
 180 185 190
 Ser Thr Val Arg Lys Pro Trp Thr Ala Val Asp Thr Ser Val Asp Gly
 195 200 205
 Arg Lys Arg Thr Phe Tyr Leu Ser Val Cys Asn Pro Leu Pro Tyr Ile
 210 215 220
 Pro Gly Cys Gln Gly Ser Ala Val Gly Ser Cys Leu Val Ser Glu Gly
 225 230 235 240
 Asn Ser Trp Asn Leu Gly Val Val Gln Met Ser Pro Gln Ala Ala Ala
 245 250 255
 Asn Gly Ser Leu Ser Ile Met Tyr Val Asn Gly Asp Lys Cys Gly Asn
 260 265 270
 Gln Arg Phe Ser Thr Arg Ile Thr Phe Glu Cys Ala Gln Ile Ser Gly
 275 280 285
 Ser Pro Ala Phe Gln Leu Gln Asp Gly Cys Glu Tyr Val Phe Ile Trp
 290 295 300
 Arg Thr Val Glu Ala Cys Pro Val Val Arg Val Glu Gly Asp Asn Cys
 305 310 315 320
 Glu Val Lys Asp Pro Arg His Gly Asn Leu Tyr Asp Leu Lys Pro Leu
 325 330 335
 Gly Leu Asn Asp Thr Ile Val Ser Ala Gly Glu Tyr Thr Tyr Tyr Phe
 340 345 350
 Arg Val Cys Gly Lys Leu Ser Ser Asp Val Cys Pro Thr Ser Asp Lys
 355 360 365
 Ser Lys Val Val Ser Ser Cys Gln Glu Lys Arg Glu Pro Gln Gly Phe
 370 375 380
 His Lys Val Ala Gly Leu Leu Thr Gln Lys Leu Thr Tyr Glu Asn Gly
 385 390 395 400
 Leu Leu Lys Met Asn Phe Thr Gly Gly Asp Thr Cys His Lys Val Tyr
 405 410 415
 Gln Arg Ser Thr Ala Ile Phe Phe Tyr Cys Asp Arg Gly Thr Gln Arg
 420 425 430
 Pro Val Phe Leu Lys Glu Thr Ser Asp Cys Ser Tyr Leu Phe Glu Trp
 435 440 445
 Arg Thr Gln Tyr Ala Cys Pro Pro Phe Asp Leu Thr Glu Cys Ser Phe
 450 455 460
 Lys Asp Gly Ala Gly Asn Ser Phe Asp Leu Ser Ser Leu Ser Arg Tyr
 465 470 475 480
 Ser Asp Asn Trp Glu Ala Ile Thr Gly Thr Gly Asp Pro Glu His Tyr
 485 490 495
 Leu Ile Asn Val Cys Lys Ser Leu Ala Pro Gln Ala Gly Thr Glu Pro
 500 505 510
 Cys Pro Pro Glu Ala Ala Ala Cys Leu Leu Gly Gly Ser Lys Pro Val
 515 520 525
 Asn Leu Gly Arg Val Arg Asp Gly Pro Gln Trp Arg Asp Gly Ile Ile
 530 535 540
 Val Leu Lys Tyr Val Asp Gly Asp Leu Cys Pro Asp Gly Ile Arg Lys
 545 550 555 560
 Lys Ser Thr Thr Ile Arg Phe Thr Cys Ser Glu Ser Gln Val Asn Ser
 565 570 575
 Arg Pro Met Phe Ile Ser Ala Val Glu Asp Cys Glu Tyr Thr Phe Ala
 580 585 590
 Trp Pro Thr Ala Thr Ala Cys Pro Met Lys Ser Asn Glu His Asp Asp
 595 600 605
 Cys Gln Val Thr Asn Pro Ser Thr Gly His Leu Phe Asp Leu Ser Ser
 610 615 620
 Leu Ser Gly Arg Ala Gly Phe Thr Ala Ala Tyr Ser Glu Lys Gly Leu

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Met Ala Arg Leu Ser Arg Pro Glu Arg Pro Asp Leu Val Phe Glu Glu
 1 5 10 15
 Glu Asp Leu Pro Tyr Glu Glu Glu Ile Met Arg Asn Gln Phe Ser Val
 20 25 30
 Lys Cys Trp Leu His Tyr Ile Glu Phe Lys Gln Gly Ala Pro Lys Pro
 35 40 45
 Arg Leu Asn Gln Leu Tyr Glu Arg Ala Leu Lys Leu Leu Pro Cys Ser
 50 55 60
 Tyr Lys Leu Trp Tyr Arg Tyr Leu Lys Ala Arg Arg Ala Gln Val Lys
 65 70 75 80
 His Arg Cys Val Thr Asp Pro Ala Tyr Glu Asp Val Asn Asn Cys His
 85 90 95
 Glu Arg Ala Phe Val Phe Met His Lys Met Pro Arg Leu Trp Leu Asp
 100 105 110
 Tyr Cys Gln Phe Leu Met Asp Gln Gly Arg Val Thr His Thr Arg Arg
 115 120 125
 Thr Phe Asp Arg Ala Leu Arg Ala Leu Pro Ile Thr Gln His Ser Arg
 130 135 140
 Ile Trp Pro Leu Tyr Leu Arg Phe Leu Arg Ser His Pro Leu Pro Glu
 145 150 155 160
 Thr Ala Val Arg Gly Tyr Arg Arg Phe Leu Lys Leu Ser Pro Glu Ser
 165 170 175
 Ala Glu Glu Tyr Ile Glu Tyr Leu Lys Ser Ser Asp Arg Leu Asp Glu
 180 185 190
 Ala Ala Gln Arg Leu Ala Thr Val Val Asn Asp Glu Arg Phe Val Ser
 195 200 205
 Lys Ala Gly Lys Ser Asn Tyr Gln Leu Trp His Glu Leu Cys Asp Leu
 210 215 220
 Ile Ser Gln Asn Pro Asp Lys Val Gln Ser Leu Asn Val Asp Ala Ile
 225 230 235 240
 Ile Arg Gly Gly Leu Thr Arg Phe Thr Asp Gln Leu Gly Lys Leu Trp
 245 250 255

Cys Ser Leu Ala Asp Tyr Tyr Ile Arg Ser Gly His Phe Glu Lys Ala
 260 265 270
 Arg Asp Val Tyr Glu Glu Ala Ile Arg Thr Val Met Thr Val Arg Asp
 275 280 285
 Phe Thr Gln Val Phe Asp Ser Tyr Ala Gln Phe Glu Glu Ser Met Ile
 290 295 300
 Ala Ala Lys Met Glu Thr Ala Ser Glu Leu Gly Arg Glu Glu Glu Asp
 305 310 315 320
 Asp Val Asp Leu Glu Leu Arg Leu Ala Arg Phe Glu Gln Leu Ile Ser
 325 330 335
 Arg Arg Pro Leu Leu Leu Asn Ser Val Leu Leu Arg Gln Asn Pro His
 340 345 350
 His Val His Glu Trp His Lys Arg Val Ala Leu His Gln Gly Arg Pro
 355 360 365
 Arg Glu Ile Ile Asn Thr Tyr Glu Ala Val Gln Thr Val Asp Pro
 370 375 380
 Phe Lys Ala Thr Gly Lys Pro His Thr Leu Trp Val Ala Phe Ala Lys
 385 390 395 400
 Phe Tyr Glu Asp Asn Gly Gln Leu Asp Asp Ala Arg Val Ile Leu Glu
 405 410 415
 Lys Ala Thr Lys Val Asn Phe Lys Gln Val Asp Asp Leu Ala Ser Val
 420 425 430
 Trp Cys Gln Cys Gly Glu Leu Glu Leu Arg His Glu Asn Tyr Asp Glu
 435 440 445
 Ala Leu Arg Leu Leu Arg Lys Ala Thr Ala Leu Pro Ala Arg Arg Ala
 450 455 460
 Glu Tyr Phe Asp Gly Ser Glu Pro Val Gln Asn Arg Val Tyr Lys Ser
 465 470 475 480
 Leu Lys Val Trp Ser Met Leu Ala Asp Leu Glu Glu Ser Leu Gly Thr
 485 490 495
 Phe Gln Ser Thr Lys Ala Val Tyr Asp Arg Ile Leu Asp Leu Arg Ile
 500 505 510
 Ala Thr Pro Gln Ile Val Ile Asn Tyr Ala Met Phe Leu Glu Glu His
 515 520 525
 Lys Tyr Phe Glu Glu Ser Phe Lys Ala Tyr Glu Arg Gly Ile Ser Leu
 530 535 540
 Phe Lys Trp Pro Asn Val Ser Asp Ile Trp Ser Thr Tyr Leu Thr Lys
 545 550 555 560
 Phe Ile Ala Arg Tyr Gly Gly Arg Lys Leu Glu Arg Ala Arg Asp Leu
 565 570 575
 Phe Glu Gln Ala Leu Asp Gly Cys Pro Pro Lys Tyr Ala Lys Thr Leu
 580 585 590
 Tyr Leu Leu Tyr Ala Gln Leu Glu Glu Trp Gly Leu Ala Arg His
 595 600 605
 Ala Met Ala Val Tyr Glu Arg Ala Thr Arg Ala Val Glu Pro Ala Gln
 610 615 620
 Gln Tyr Asp Met Phe Asn Ile Tyr Ile Lys Arg Ala Ala Glu Ile Tyr
 625 630 635 640
 Gly Val Thr His Thr Arg Gly Ile Tyr Gln Lys Ala Ile Glu Val Leu
 645 650 655
 Ser Asp Glu His Ala Arg Glu Met Cys Leu Arg Phe Ala Asp Met Glu
 660 665 670
 Cys Lys Leu Gly Glu Ile Asp Arg Ala Arg Ala Ile Tyr Ser Phe Cys
 675 680 685
 Ser Gln Ile Cys Asp Pro Arg Thr Thr Gly Ala Phe Trp Gln Thr Trp
 690 695 700
 Lys Asp Phe Glu Val Arg His Gly Asn Glu Asp Thr Ile Lys Glu Met
 705 710 715 720
 Leu Arg Ile Arg Arg Ser Val Gln Ala Thr Tyr Asn Thr Gln Val Asn
 725 730 735
 Phe Met Ala Ser Gln Met Leu Lys Val Ser Gly Ser Ala Thr Gly Thr
 740 745 750
 Val Ser Asp Leu Ala Pro Gly Gln Ser Gly Met Asp Asp Met Lys Leu
 755 760 765
 Leu Glu Gln Arg Ala Glu Gln Leu Ala Ala Glu Ala Glu Arg Asp Gln
 770 775 780
 Pro Leu Arg Ala Gln Ser Lys Ile Leu Phe Val Arg Ser Asp Ala Ser
 785 790 795 800
 Arg Glu Glu Leu Ala Glu Leu Ala Gln Gln Val Asn Pro Glu Glu Ile
 805 810 815
 Gln Leu Gly Glu Asp Glu Asp Glu Asp Glu Met Asp Leu Glu Pro Asn
 820 825 830
 Glu Val Arg Leu Glu Gln Gln Ser Val Pro Ala Ala Val Phe Gly Ser

835 840 845
Leu Lys Glu Asp
850

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Met	Phe	Ser	Ala	Leu	Lys	Lys	Leu	Val	Gly	Ser	Asp	Gln	Ala	Pro	Gly
1				5				10							15
Arg	Asp	Lys	Asn	Ile	Pro	Ala	Gly	Leu	Gln	Ser	Met	Asn	Gln	Ala	Leu
				20				25							30
Gln	Arg	Arg	Phe	Ala	Lys	Gly	Val	Gln	Tyr	Asn	Met	Lys	Ile	Val	Ile
				35				40							45
Arg	Gly	Asp	Arg	Asn	Thr	Gly	Lys	Thr	Ala	Leu	Trp	His	Arg	Leu	Gln
					50		55				60				
Gly	Arg	Pro	Phe	Val	Glu	Glu	Tyr	Ile	Pro	Thr	Gln	Glu	Ile	Gln	Val
				65		70		75							80
Thr	Ser	Ile	His	Trp	Ser	Tyr	Lys	Thr	Thr	Asp	Asp	Ile	Val	Lys	Val
					85			90							95
Glu	Val	Trp	Asp	Val	Val	Asp	Lys	Gly	Lys	Cys	Lys	Lys	Arg	Gly	Asp
				100			105								110
Gly	Leu	Lys	Met	Glu	Asn	Asp	Pro	Gln	Glu	Xaa	Glu	Ser	Glu	Met	Ala
				115			120								125
Leu	Asp	Ala	Glu	Phe	Leu	Asp	Val	Tyr	Lys	Asn	Cys	Asn	Gly	Val	Val
				130		135			140						
Met	Met	Phe	Asp	Ile	Thr	Lys	Gln	Trp	Thr	Phe	Asn	Tyr	Ile	Leu	Arg
				145		150			155						160
Glu	Leu	Pro	Lys	Val	Pro	Thr	His	Val	Pro	Val	Cys	Val	Leu	Gly	Asn
					165			170							175
Tyr	Arg	Asp	Met	Gly	Glu	His	Arg	Val	Ile	Leu	Pro	Asp	Asp	Val	Arg
				180			185								190
Asp	Phe	Ile	Asp	Asn	Leu	Asp	Arg	Pro	Pro	Gly	Ser	Ser	Tyr	Phe	Arg
				195			200								205
Tyr	Ala	Glu	Ser	Ser	Met	Lys	Asn	Ser	Phe	Gly	Leu	Lys	Tyr	Leu	His
				210		215			220						
Lys	Phe	Phe	Asn	Ile	Pro	Phe	Leu	Gln	Leu	Gln	Arg	Glu	Thr	Leu	Leu
				225		230			235						240
Arg	Gln	Leu	Glu	Thr	Asn	Gln	Leu	Asp	Met	Asp	Ala	Thr	Leu	Glu	Glu
					245			250							255
Leu	Ser	Val	Gln	Gln	Glu	Thr	Glu	Asp	Gln	Asn	Tyr	Gly	Ile	Phe	Leu
				260			265								270
Glu	Met	Met	Glu	Ala	Arg	Ser	Arg	Gly	His	Ala	Ser	Pro	Leu	Ala	Ala
				275		280			285						
Asn	Gly	Gln	Ser	Pro	Ser	Pro	Gly	Ser	Gln	Ser	Pro	Val	Leu	Pro	Ala
				290		295			300						
Pro	Ala	Val	Ser	Thr	Gly	Ser	Ser	Ser	Pro	Gly	Thr	Pro	Gln	Pro	Ala
				305		310			315						320
Pro	Gln	Leu	Pro	Ley	Asn	Ala	Ala	Pro	Pro	Ser	Ser	Val	Pro	Pro	Val
					325			330							335
Pro	Pro	Ser	Glu	Ala	Leu	Pro	Pro	Pro	Ala	Cys	Pro	Ser	Ala	Pro	Ala
				340			345								350
Pro	Arg	Arg	Ser	Ile	Ile	Ser	Arg	Leu	Phe	Gly	Thr	Ser	Pro	Ala	Thr
				355			360			365					
Glu	Ala	Ala	Pro	Pro	Pro	Pro	Glu	Pro	Val	Pro	Ala	Ala	Gln	Gly	Pro
				370		375			380						
Ala	Thr	Val	Gln	Ser	Val	Glu	Asp	Phe	Val	Pro	Asp	Asp	Arg	Leu	-Asp
				385		390			395						400
Arg	Ser	Phe	Leu	Glu	Asp	Thr	Thr	Pro	Ala	Arg	Asp	Glu	Lys	Val	
					405			410							415
Gly	Ala	Lys	Ala	Ala	Gln	Gln	Asp	Ser	Asp	Ser	Asp	Gly	Glu	Ala	Leu
				420			425								430
Gly	Gly	Asn	Pro	Met	Val	Ala	Gly	Phe	Gln	Asp	Asp	Val	Asp	Leu	Glu
				435			440			445					
Asp	Gln	Pro	Arg	Gly	Ser	Pro	Pro	Leu	Pro	Ala	Gly	Pro	Val	Pro	Ser
				450		455			460						

Gln Asp Ile Thr Leu Ser Ser Glu Glu Glu Ala Glu Val Ala Ala Pro
465 470 475 480
Thr Lys Gly Pro Ala Pro Ala Pro Gln Gln Cys Ser Glu Pro Glu Thr
485 490 495
Lys Trp Ser Ser Ile Pro Ala Ser Lys Pro Arg Arg Gly Thr Ala Pro
500 505 510
Thr Arg Thr Ala Ala Pro Pro Irp Pro Gly Gly Val Ser Val Arg Thr
515 520 525
Gly Pro Glu Lys Arg Ser Ser Thr Arg Pro Pro Ala Glu Met Glu Pro
530 535 540
Gly Lys Gly Glu Gln Ala Ser Ser Ser Glu Ser Asp Pro Glu Gly Pro
545 550 555 560
Ile Ala Ala Gln Met Leu Ser Phe Val Met Asp Asp Pro Asp Phe Glu
565 570 575
Ser Glu Gly Ser Asp Thr Gln Arg Arg Ala Asp Asp Phe Pro Val Arg
580 585 590
Asp Asp Pro Ser Asp Val Thr Asp Glu Asp Glu Gly Pro Ala Glu Pro
595 600 605
Pro Pro Pro Pro Lys Leu Pro Leu Pro Ala Phe Arg Leu Lys Asn Asp
610 615 620
Ser Asp Leu Phe Gly Leu Gly Leu Glu Ala Gly Pro Lys Glu Ser
625 630 635 640
Ser Glu Glu Gly Lys Glu Gly Lys Thr Pro Ser Lys Glu Lys Lys Lys
645 650 655
Lys Thr Lys Ser Phe Ser Arg Val Leu Leu Glu Arg Pro Arg Ala His
660 665 670
Arg Phe Ser Thr Arg Val Gly Tyr Gln Val Ser Val Pro Asn Ser Pro
675 680 685
Tyr Ser Glu Ser Tyr
690